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(74) Agent: SPRUNGER, Suzanne, A.; Genetics Institute, Inc., 87 CambridgePark Drive, Cambridge, MA 02140 (US).			Published <i>Without international search report and to be republished upon receipt of that report.</i>
(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (sESTs)			
(57) Abstract Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.			



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(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (sESTs) (57) Abstract Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.		

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SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

FIELD OF THE INVENTION

5 The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

10 Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of target organisms which are not actually expressed wastes substantial effort on areas not likely
15 to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they were transcribed.

20 Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect. Since the EST approach theoretically identifies all expressed proteins, it produces an EST
25 library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators searching for secreted proteins because they must separate the secreted "wheat" from the non-
30 secreted "chaff", wasting effort and resources in the process.

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Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted proteins,
5 namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

SUMMARY OF THE INVENTION

The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

In other embodiments, the present invention provides an isolated polynucleotide
 consisting of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

20 In further embodiments, the present invention provides an isolated polynucleotide
consisting essentially of a nucleotide sequence selected from the group consisting of:

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or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide
 comprising a nucleotide sequence which hybridizes to a sequence selected from the group
 30 consisting of:

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NO:1493, SEQ ID NO:1494, SEQ ID NO:1495, SEQ ID NO:1496, SEQ ID
NO:1497, SEQ ID NO:1498, SEQ ID NO:1499, and SEQ ID NO:1500;

or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described
5 polynucleotides.

DETAILED DESCRIPTION

The nucleotide sequences of the sESTs of the present invention are reported in the
Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each
10 SEQ ID NO: in the Sequence Listing.

Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.)
followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

15	1	B11	21	C3	41	C639	61	D148
	2	B18	22	C32	42	C641	62	D154
	3	B21	23	C141	43	C642	63	D167
	4	B26	24	C143	44	C645	64	D179
	5	B40	25	C180	45	D4	65	D188
20	6	B115	26	C195	46	D7	66	D196
	7	B121	27	C293	47	D14	67	D200
	8	B124	28	C312	48	D15	68	D203
	9	B125	29	C539	49	D27	69	D233
	10	B142	30	C544	50	D68	70	D252
25	11	B196	31	C547	51	D69	71	D286
	12	B208	32	C571	52	D81	72	D303
	13	B224	33	C604	53	D100	73	D304
	14	B227	34	C607	54	D101	74	D305
	15	B232	35	C608	55	D104	75	D310
30	16	B236	36	C610	56	D105	76	D311
	17	B238	37	C617	57	D115	77	D318
	18	B255	38	C626	58	D121	78	D327
	19	C1	39	C627	59	D133	79	D329
	20	C2	40	C636	60	D143	80	E1

	81	E4	115	H291	149	J139	183	M141
	82	E5	116	H306	150	J143	184	M152
	83	E11	117	H383	151	J156	185	M194
	84	E12	118	H426	152	J168	186	M230
5	85	E14	119	H438	153	J297	187	M273
	86	E18	120	H541	154	J317	188	M292
	87	G1	121	H545	155	J322	189	M301
	88	G12	122	H657	156	J422	190	M313
	89	G16	123	H698	157	J435	191	M328
10	90	G20	124	H758	158	J509	192	M338
	91	G21	125	H770	159	J512	193	O7
	92	G26	126	H849	160	J532	194	O47
	93	G31	127	H920	161	J546	195	O67
	94	G40	128	H978	162	J598	196	O75
15	95	G46	129	H999	163	J635	197	O99
	96	G53	130	H1004	164	J638	198	O135
	97	G55	131	H1010	165	J708	199	O139
	98	G58	132	H1045	166	J731	200	O268
	99	G68	133	H1052	167	M4	201	O276
20	100	G85	134	H1075	168	M6	202	O289
	101	G86	135	H1096	169	M43	203	O338
	102	G99	136	H1116	170	M60	204	O349
	103	G103	137	H1165	171	M68	205	O351
	104	G107	138	H1301	172	M71	206	O372
25	105	G108	139	H1408	173	M88	207	O386
	106	G112	140	H1413	174	M97	208	O417
	107	G114	141	H1456	175	M100	209	O418
	108	H45	142	I5	176	M114	210	O463
	109	H162	143	I28	177	M120	211	S10
30	110	H165	144	I32	178	M121	212	S34
	111	H171	145	J5	179	M125	213	S70
	112	H174	146	J54	180	M126	214	S169
	113	H225	147	J66	181	M128	215	S185
	114	H236	148	J135	182	M137	216	S195

	217	AA20	251	AJ6	285	AM72	319	AP137
	218	AA35	252	AJ8	286	AM93	320	AP76
	219	AB10	253	AJ52	287	AK679	321	AP87
	220	AA240	254	AJ53	288	AK684	322	AP90
5	221	AA244	255	AJ54	289	AK699	323	AP150
	222	AA246	256	AJ78	290	AM155	324	AP159
	223	AA287	257	AJ80	291	AM167	325	AP160
	224	AA299	258	AK368	292	AM207	326	AP162
	225	AA318	259	AJ127	293	AM217	327	AP168
10	226	AB45	260	AJ142	294	AM224	328	AP179
	227	AA36	261	AJ143	295	AM226	329	AP197
	228	AA363	262	AC339	296	AM235	330	AP215
	229	AA365	263	AC370	297	AM259	331	AP224
	230	AA351	264	AL14	298	AM266	332	AP226
15	231	AB290	265	AK401	299	AM267	333	AP242
	232	AC41	266	AK438	300	AM277	334	AP250
	233	AC18	267	AK583	301	AM279	335	AQ11
	234	AC175	268	AK585	302	AC387	336	AQ2
	235	AC114	269	AK598	303	AC395	337	AQ21
20	236	AC111	270	AK604	304	AC410	338	AQ23
	237	AC100	271	AK609	305	AC412	339	AQ3
	238	AC222	272	AK620	306	AC423	340	AQ34
	239	AC325	273	AM10	307	AJ146	341	AQ5
	240	AI44	274	AM104	308	AJ147	342	AR15
25	241	AI6	275	AM123	309	AJ156	343	AR22
	242	AI86	276	AM137	310	AJ168	344	AR28
	243	AJ1	277	AM15	311	AJ169	345	AR3
	244	AJ10	278	AM16	312	AJ172	346	AR34
	245	AJ13	279	AM30	313	AJ173	347	AR42
30	246	AJ15	280	AM38	314	AJ174	348	AR54
	247	AJ20	281	AM39	315	AK528	349	AR61
	248	AJ21	282	AM42	316	AP116	350	AM282
	249	AJ26	283	AM46	317	AP120	351	AM307
	250	AJ27	284	AM66	318	AP135	352	AM349

	353	AM372	387	AR310	421	AM616	455	AM921
	354	AM392	388	AR323	422	AM622	456	AM931
	355	AM400	389	AR324	423	AM625	457	AM973
	356	AM430	390	AR325	424	AM666	458	AM996
5	357	AP11	391	AR349	425	AM686	459	AS56
	358	AP2	392	AR360	426	AM704	460	AS61
	359	AP56	393	AR364	427	AM726	461	AS63
	360	AP57	394	AR400	428	AM728	462	AS65
	361	AP58	395	AR415	429	AM735	463	AS83
10	362	AP60	396	AR417	430	AM741	464	AS85
	363	AP67	397	AM558	431	AM742	465	AS86
	364	AP7	398	AM566	432	AM754	466	AS88
	365	AQ53	399	AM600	433	AM781	467	AT107
	366	AQ54	400	AR420	434	AM795	468	AT111
15	367	AQ61	401	AR437	435	AM814	469	AT138
	368	AQ64	402	AR440	436	AM833	470	AT140
	369	AQ71	403	AR446	437	AM838	471	AT142
	370	AQ73	404	AR450	438	AT16	472	AT146
	371	AQ83	405	AR452	439	AT19	473	AT151
20	372	AM1075	406	AR455	440	AT20	474	AT157
	373	AM1076	407	AR463	441	AT4	475	AT181
	374	AM1083	408	AR464	442	AT53	476	AT97
	375	AR100	409	AR467	443	AT63	477	AS239
	376	AR69	410	AR474	444	AT64	478	AT226
25	377	AM1017	411	AR475	445	AT74	479	AT259
	378	AM1032	412	AS15	446	AT94	480	AT260
	379	AM1036	413	AS20	447	AT95	481	AT265
	380	AM1045	414	AS23	448	AM1000	482	AT280
	381	AM1060	415	AS31	449	AM856	483	AT340
30	382	AM1067	416	AS47	450	AM885	484	AT351
	383	AR253	417	AS48	451	AM889	485	AT352
	384	AK642	418	AS7	452	AM892	486	AT356
	385	AK647	419	AM610	453	AM910	487	AT359
	386	AK650	420	AM614	454	AM918	488	AT361

	489	AS252	523	AU161	557	AW106	591	BE28
	490	AS263	524	AU164	558	AW107	592	BE3
	491	AS264	525	AZ285	559	AW109	593	BE34
	492	AS268	526	AZ286	560	AW133	594	BE9
5	493	AS271	527	AZ287	561	AW140	595	AZ12
	494	AS294	528	AZ290	562	AW92	596	AZ22
	495	AS301	529	AZ188	563	AW95	597	AZ32
	496	AS330	530	AZ191	564	AW98	598	AZ45
	497	AS144	531	AZ204	565	BA185	599	AZ46
10	498	AS152	532	AZ219	566	BA204	600	BF143
	499	AS157	533	AW170	567	BA210	601	BF146
	500	AS162	534	AW176	568	BA226	602	BF157
	501	AS164	535	AW178	569	BG1	603	BF160
	502	AS167	536	AW179	570	BG13	604	BF169
15	503	AS180	537	AW182	571	BG3	605	BF171
	504	AS186	538	AW185	572	BG33	606	BF176
	505	AS187	539	AW189	573	BG36	607	BF178
	506	AU36	540	AW192	574	BG37	608	AS196
	507	AU39	541	AW194	575	BG40	609	AS202
20	508	AU43	542	AW199	576	BG43	610	AS209
	509	AU47	543	AW222	577	BG48	611	AS216
	510	AU50	544	AW231	578	BG58	612	AS230
	511	AU59	545	AZ261	579	BG72	613	AS232
	512	AU71	546	AZ264	580	BG73	614	AX101
25	513	AU101	547	AZ302	581	BF101	615	AX104
	514	AU102	548	AZ303	582	BF132	616	AX107
	515	AU105	549	AK649	583	AZ69	617	AX109
	516	AU106	550	AK663	584	BD51	618	AX122
	517	AU107	551	AR336	585	BD53	619	AX124
30	518	AU115	552	AR356	586	BD65	620	AX127
	519	AU118	553	AR398	587	BD66	621	AX128
	520	AU122	554	AR399	588	BD73	622	AX130
	521	AU138	555	AM1016	589	BD77	623	AX132
	522	AU139	556	AW105	590	BD80	624	AX136

	625	AX137	659	BG274	693	AW33	727	BG504
	626	AX143	660	BG276	694	AW36	728	BG510
	627	AX146	661	AX12	695	AW47	729	BG511
	628	AX51	662	AX17	696	AW49	730	BG513
5	629	AX55	663	AX256	697	AW52	731	BG516
	630	AX56	664	AX30	698	AW60	732	BG518
	631	AX60	665	AX32	699	AW66	733	BG526
	632	AX65	666	AX34	700	AW76	734	BG528
	633	AX78	667	AX49	701	AY241	735	BG552
10	634	AX80	668	AX6	702	AY259	736	BG553
	635	AX81	669	AX8	703	AY268	737	BG556
	636	AX92	670	AZ180	704	BA123	738	AX309
	637	AX97	671	BG191	705	BA134	739	AX315
	638	AX98	672	BG193	706	BA170	740	AX318
15	639	AX99	673	BG199	707	BA176	741	AY186
	640	AZ109	674	BG201	708	BA178	742	AY190
	641	AZ114	675	BG219	709	BA179	743	AY200
	642	BF286	676	BG220	710	BA216	744	AY208
	643	BF290	677	BG221	711	BA233	745	AY211
20	644	BF314	678	BG225	712	BD372	746	AY283
	645	BG236	679	BG228	713	BD375	747	AY289
	646	BG237	680	BG442	714	BD379	748	AY304
	647	BG240	681	BG449	715	BD380	749	AY307
	648	BG241	682	BG457	716	BD403	750	AY318
25	649	BG248	683	BG458	717	BD407	751	AY333
	650	BG249	684	BG461	718	BD409	752	AY334
	651	BG250	685	BG465	719	BD413	753	AY342
	652	BG251	686	BG467	720	BD414	754	AY358
	653	BG255	687	BG471	721	BG481	755	AY362
30	654	BG260	688	BG59	722	BG482	756	BF190
	655	BG267	689	AW12	723	BG492	757	BF191
	656	BG271	690	AW22	724	BG494	758	BF193
	657	BG272	691	AW24	725	BG495	759	BF197
	658	BG273	692	AW32	726	BG503	760	BF208

	761	BF211	795	BG373	829	BD174	863	BI17
	762	BF216	796	BG374	830	BD176	864	BI2
	763	BF221	797	BG379	831	BD177	865	BI24
	764	BF227	798	BG386	832	BD178	866	BI25
5	765	BF228	799	BG388	833	BD183	867	BI3
	766	BF245	800	BG389	834	BE50	868	BI36
	767	BF250	801	BG391	835	BE64	869	BI37
	768	BF258	802	BG393	836	BE89	870	BI39
	769	BF259	803	BG396	837	BG490	871	BI40
10	770	BF263	804	BG409	838	BG491	872	BI41
	771	BF270	805	BG411	839	BG501	873	BI46
	772	BF273	806	BG414	840	BG502	874	BM1
	773	BG280	807	BG420	841	BG512	875	BM17
	774	BG283	808	HW105	842	BG532	876	BM4
15	775	BG284	809	BB54	843	BK162	877	BM41
	776	BG288	810	BD101	844	BK165	878	BM46
	777	BG296	811	BD104	845	BK167	879	BM69
	778	BG305	812	BD107	846	BK171	880	BM88
	779	BG306	813	BD109	847	BK179	881	BM90
20	780	BG309	814	BD119	848	BK180	882	BA106
	781	BG324	815	BD121	849	BK183	883	BA12
	782	BG327	816	BD127	850	BK186	884	BA32
	783	BG329	817	BD128	851	BK194	885	BA38
	784	BG332	818	BD132	852	BK200	886	BA40
25	785	BG334	819	BD136	853	BK206	887	BA71
	786	BG335	820	BD137	854	BK216	888	BA79
	787	BG350	821	BD140	855	BK231	889	BA8
	788	BG356	822	BD144	856	BK232	890	BA88
	789	BG357	823	BD151	857	BK236	891	BA90
30	790	BG363	824	BD154	858	BK237	892	BA91
	791	BG365	825	BD164	859	BK241	893	BA98
	792	BG366	826	BD165	860	BK243	894	BK15
	793	BG368	827	BD169	861	BK246	895	BK17
	794	BG372	828	BD170	862	BK253	896	BK24

	897	BK257	931	AY428	965	BK146	999	BG139
	898	BK26	932	AY437	966	BK155	1000	BG140
	899	BK260	933	AY440	967	BK158	1001	BG141
	900	BK265	934	AY442	968	BK75	1002	BG142
5	901	BK270	935	AY449	969	BK78	1003	BG145
	902	BK271	936	AY457	970	BK92	1004	BG148
	903	BK280	937	AY470	971	BK93	1005	BG151
	904	BK284	938	AY487	972	BK95	1006	BG156
	905	BK286	939	AY489	973	BK96	1007	BG158
10	906	BK29	940	AY511	974	BM101	1008	BG160
	907	BK291	941	BE153	975	BM117	1009	BG168
	908	BK295	942	BF327	976	BM124	1010	BG170
	909	BK296	943	BI64	977	BM139	1011	BG171
	910	BK299	944	BI66	978	BM154	1012	BG172
15	911	BK304	945	BI75	979	BM155	1013	BG173
	912	BK307	946	BI80	980	BM158	1014	BG93
	913	BK308	947	BI81	981	BM94	1015	BG95
	914	BK339	948	BI82	982	AY102	1016	BI102
	915	BK34	949	BI86	983	AY107	1017	BI103
20	916	BK343	950	BI87	984	AY122	1018	BI107
	917	BK40	951	BI88	985	AY131	1019	BI110
	918	BK41	952	BI91	986	AY137	1020	BI114
	919	BK48	953	BI92	987	AY140	1021	BI117
	920	BK49	954	BK102	988	AY147	1022	BI120
25	921	BK57	955	BK105	989	AY157	1023	BI122
	922	BK59	956	BK107	990	AY160	1024	BI124
	923	BK61	957	BK112	991	AY183	1025	BI126
	924	BK68	958	BK114	992	AY93	1026	BI127
	925	BL341	959	BK115	993	BG102	1027	BI129
30	926	AY398	960	BK117	994	BG104	1028	BI133
	927	AY406	961	BK120	995	BG112	1029	BI139
	928	AY407	962	BK130	996	BG125	1030	BI150
	929	AY408	963	BK134	997	BG132	1031	BI164
	930	AY421	964	BK142	998	BG137	1032	BI97

	1033	BI98	1067	BQ58	1101	BO71	1135	BL209
	1034	BI99	1068	BD189	1102	BO87	1136	BL210
	1035	BS1	1069	BD194	1103	BO9	1137	BL211
	1036	BS54	1070	BD199	1104	BD235	1138	BL219
5	1037	BS58	1071	BD200	1105	BD240	1139	BL220
	1038	BS81	1072	BD201	1106	BD241	1140	BL229
	1039	BS89	1073	BD208	1107	BD244	1141	BL230
	1040	BH100	1074	BD209	1108	BD247	1142	BL243
	1041	BH106	1075	BD213	1109	BD251	1143	BL247
10	1042	BH111	1076	BD214	1110	BD257	1144	BL249
	1043	BH123	1077	BD222	1111	BD260	1145	BL255
	1044	BH131	1078	BH19	1112	BD262	1146	BL257
	1045	BH157	1079	BH195	1113	BD265	1147	BL271
	1046	BH297	1080	BH2	1114	BD268	1148	BL274
15	1047	BH306	1081	BH227	1115	BD522	1149	BL30
	1048	BH309	1082	BH272	1116	BD538	1150	BL67
	1049	BH316	1083	BH276	1117	BD544	1151	BL73
	1050	BH323	1084	BH281	1118	BD548	1152	BL89
	1051	BH339	1085	BH41	1119	BD561	1153	BD420
20	1052	BH365	1086	BH51	1120	BL147	1154	BD423
	1053	BH389	1087	BH66	1121	BL15	1155	BD426
	1054	BH392	1088	BH7	1122	BL152	1156	BD427
	1055	BJ54	1089	BH87	1123	BL156	1157	BD428
	1056	BJ62	1090	BH90	1124	BL160	1158	BD438
25	1057	BJ66	1091	BJ20	1125	BL178	1159	BD441
	1058	BJ67	1092	BJ27	1126	BL179	1160	BD445
	1059	BJ69	1093	BJ29	1127	BL183	1161	BD473
	1060	BJ70	1094	BJ38	1128	BL185	1162	BD486
	1061	BJ75	1095	BJ39	1129	BL186	1163	BD489
30	1062	BJ76	1096	BJ9	1130	BL187	1164	BD492
	1063	BJ78	1097	BO11	1131	BL194	1165	BD512
	1064	BJ87	1098	BO20	1132	BL196	1166	BL106
	1065	BQ20	1099	BO4	1133	BL201	1167	BL310
	1066	BQ3	1100	BO52	1134	BL205	1168	BN1

	1169	BN107	1203	BD351	1237	BN351	1271	BP22
	1170	BN12	1204	BN189	1238	BN354	1272	BP24
	1171	BN130	1205	BN201	1239	BN365	1273	BP25
	1172	BN132	1206	BN212	1240	BN422	1274	BT99
5	1173	BN133	1207	BN280	1241	BN425	1275	BP28
	1174	BN139	1208	BN284	1242	BN439	1276	BP3
	1175	BN141	1209	BN329	1243	BN460	1277	BP4
	1176	BN153	1210	BN331	1244	BN461	1278	BP43
	1177	BN156	1211	BN591	1245	BN463	1279	BP47
10	1178	BN171	1212	BO153	1246	BN472	1280	BP504
	1179	BN174	1213	BO157	1247	BN473	1281	BP506
	1180	BN180	1214	BO159	1248	BO100	1282	BP508
	1181	BN246	1215	BO166	1249	BO107	1283	BP521
	1182	BN267	1216	BO178	1250	BO114	1284	BP528
15	1183	BN268	1217	BO189	1251	BO121	1285	BP530
	1184	BN33	1218	BO194	1252	BO126	1286	BP532
	1185	BN40	1219	BO210	1253	BO133	1287	BP537
	1186	BN48	1220	BO212	1254	BO137	1288	BP544
	1187	BN5	1221	BO213	1255	BO398	1289	BP545
20	1188	BN563	1222	BO218	1256	BO399	1290	BP55
	1189	BN65	1223	BO226	1257	BO401	1291	BP567
	1190	BN69	1224	BO279	1258	BO432	1292	BP569
	1191	BN81	1225	BO301	1259	BO528	1293	BP57
	1192	BN97	1226	BO323	1260	BO535	1294	BP590
25	1193	BN99	1227	BO358	1261	BO538	1295	BP61
	1194	BD286	1228	BO365	1262	BO549	1296	BP70
	1195	BD288	1229	BO385	1263	BO551	1297	BP71
	1196	BD297	1230	BO250	1264	BO93	1298	BP780
	1197	BD316	1231	BO254	1265	BP101	1299	BP783
30	1198	BD317	1232	BO256	1266	BP118	1300	BP784
	1199	BD321	1233	BO260	1267	BP121	1301	BP791
	1200	BD327	1234	BO261	1268	BP15	1302	BP797
	1201	BD335	1235	BO273	1269	BP19	1303	BP806
	1202	BD339	1236	BN342	1270	BP21	1304	BP809

	1305	BP810	1339	BV243	1373	CC71	1407	BR572
	1306	BP813	1340	BV248	1374	CC76	1408	BR559
	1307	BP814	1341	BV250	1375	CC78	1409	BR538
	1308	BP815	1342	BV259	1376	CC81	1410	BR537
5	1309	BP820	1343	BV273	1377	CC89	1411	BR533
	1310	BP84	1344	BV275	1378	CD124	1412	BR500
	1311	BP919	1345	BV49	1379	CD128	1413	BR48
	1312	BP925	1346	BV51	1380	CD140	1414	BR475
	1313	BQ115	1347	BV66	1381	CD145	1415	BR436
10	1314	BQ129	1348	BV70	1382	CD146	1416	BR434
	1315	BS116	1349	BV71	1383	CD173	1417	BR4
	1316	BT101	1350	BV72	1384	CD194	1418	BR346
	1317	BT133	1351	BV73	1385	CD31	1419	BR342
	1318	BT139	1352	BV88	1386	CD50	1420	BR338
15	1319	BT33	1353	BW345	1387	CF50	1421	BR333
	1320	BT4	1354	CB25	1388	CF62	1422	BR332
	1321	BW13	1355	CB3	1389	CF78	1423	BR212
	1322	BW18	1356	CB30	1390	CF85	1424	BR195
	1323	BW2	1357	CB37	1391	CF89	1425	BR194
20	1324	BW51	1358	CC144	1392	BR814	1426	BR19
	1325	BW61	1359	CC145	1393	BR782	1427	BR141
	1326	BW83	1360	CC149	1394	BR778	1428	BR122
	1327	BV185	1361	CC153	1395	BR77	1429	BR107
	1328	BV195	1362	CC162	1396	BR767	1430	BR1010
25	1329	BV200	1363	CC25	1397	BR758	1431	BR101
	1330	BV202	1364	CC31	1398	BR733	1432	BR1008
	1331	BV204	1365	CC322	1399	BR719	1433	BQ135
	1332	BV206	1366	CC39	1400	BR711	1434	BP913
	1333	BV210	1367	CC397	1401	BR71	1435	BP911
30	1334	BV212	1368	CC403	1402	BR63	1436	BP897
	1335	BV227	1369	CC46	1403	BR616	1437	BP895
	1336	BV238	1370	CC50	1404	BR610	1438	BP894
	1337	BV239	1371	CC59	1405	BR607	1439	BP893
	1338	BV241	1372	CC69	1406	BR595	1440	BP884

	1441	BP883	1475	BU65
	1442	BP875	1476	BU68
	1443	BP870	1477	BU76
	1444	BP859	1478	BV106
5	1445	BP837	1479	BV112
	1446	BP833	1480	BV123
	1447	BP499	1481	BV124
	1448	BP492	1482	BV126
	1449	BP488	1483	BV128
10	1450	BP484	1484	BV131
	1451	BP483	1485	BV133
	1452	BP481	1486	BV134
	1453	BP475	1487	BV135
	1454	BN418	1488	BV138
15	1455	BN415	1489	BV139
	1456	BN405	1490	BV140
	1457	BN394	1491	BV141
	1458	BN390	1492	BV145
	1459	BN387	1493	BV15
20	1460	BN379	1494	BV158
	1461	BN377	1495	BV160
	1462	BR84	1496	BV172
	1463	BR853	1497	BV180
	1464	BR854	1498	BV21
25	1465	BR884	1499	BV27
	1466	BT160	1500	BV29
	1467	BU165		
	1468	BU29		
	1469	BU44		
30	1470	BU45		
	1471	BU53		
	1472	BU57		
	1473	BU6		
	1474	BU60		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selectin "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins which are transported across the membrane of the endoplasmic reticulum.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification
5 and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that
10 the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making
15 suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the
20 polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions,
25 most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

	Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [†]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
5	A	DNA:DNA	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	DNA:DNA	< 50	T _B *; 1xSSC	T _B *; 1xSSC
	C	DNA:RNA	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	DNA:RNA	< 50	T _D *; 1xSSC	T _D *; 1xSSC
	E	RNA:RNA	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
10	F	RNA:RNA	< 50	T _F *; 1xSSC	T _F *; 1xSSC
	G	DNA:DNA	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	DNA:DNA	< 50	T _H *; 4xSSC	T _H *; 4xSSC
	I	DNA:RNA	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	DNA:RNA	< 50	T _J *; 4xSSC	T _J *; 4xSSC
15	K	RNA:RNA	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	RNA:RNA	< 50	T _L *; 2xSSC	T _L *; 2xSSC
	M	DNA:DNA	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	DNA:DNA	< 50	T _N *; 6xSSC	T _N *; 6xSSC
	O	DNA:RNA	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
20	P	DNA:RNA	< 50	T _P *; 6xSSC	T _P *; 6xSSC
	Q	RNA:RNA	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	RNA:RNA	< 50	T _R *; 4xSSC	T _R *; 4xSSC

‡: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

*: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, T_m(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T_m(°C) = 81.5 + 16.6(log [Na⁺]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na⁺] is the concentration of sodium ions in the hybridization buffer ([Na⁺] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA

Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention
5 may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

10 The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or
15 which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding
20 protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related
25 DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-
30 DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

- and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 -
- 5 Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

- Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in:
- 10 *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun.
- 15 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

- A protein of the present invention may also exhibit immune stimulating or immune
- 20 suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may
- 25 be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course,
- 30 in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other
5 conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune
10 response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from
15 immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing
20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys
25 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the
30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient
5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding
10 a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably
15 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor
20 cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection
25 *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or
30 which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, *Immunologic studies in Humans*); Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Herrmann et al., *Proc. Natl. Acad. Sci. USA* 78:2488-2492, 1981; Herrmann et al., *J. Immunol.* 128:1968-1974, 1982; Handa et al., *J. Immunol.* 135:1564-1572, 1985; Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bowman et al., *J. Virology* 61:1992-1998; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Brown et al., *J. Immunol.* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J. Immunol.* 144:3028-3033, 1990; and Assays for B cell function: *In vitro* antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro* assays for Mouse Lymphocyte Function 3.1-

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

5 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

10 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma
15 induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of
20 progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the
25 protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein
30 may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured
5 by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

10 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

15 Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention,
20 alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may
25 be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; Vale

et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

5 A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide
10 particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can
15 stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

20 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one
25 cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et
30 al. APMIS 103:140-146, 1995; Muller et al. Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

10 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., *J. Clin. Pharmacol.* 26:131-140, 1986; Burdick et al., *Thrombosis Res.* 45:413-419, 1987; Humphrey et al., *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

15 Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

25 A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., *Proc. Natl. Acad. Sci. USA* 84:6864-6868, 1987; Bierer et al., *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein et al., *J. Exp. Med.*

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169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or
10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality,
15 arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

20 In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor
25 precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

30 A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

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ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

5 The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, 10 diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

15 As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, 20 administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

 In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a 25 mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either 30 simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous
5 administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an
10 adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain
15 physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

20 When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical
25 composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers,
30 antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 mg to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also
5 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and
10 cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices
15 for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such
20 as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

25 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

30 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
AI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
AZ	Human	Colon	Caco-2 Adenocarcinoma
B	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1or2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	PeripheralBloodMononuclearCell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	SalivaryGland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	PeripheralBloodMononuclearCell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

DL	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human	Lung CA	Adult Lung CA
FK	Human	Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
H	Human	Blood	PeripheralBloodMononuclearCell

HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
HH	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
HO	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID	Human	Muscle	N/A
IE	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61yrs., pool of 11
IH	Human	Muscle	N/A
II	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IP	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
IT	Human	Brain Thalamu	Adult Brain Thalamus

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jacobs, Kenneth
McCoy, John
LaVallie, Edward
Racie, Lisa
Merberg, David
Treacy, Maurice
Spaulding, Vikki
Agostino, Michael
- (ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS
- (iii) NUMBER OF SEQUENCES: 1500
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSE: Genetics Institute, Inc.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: Massachusetts
 - (E) COUNTRY: U.S.A
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy Disk
 - (B) COMPUTER: IBM PC Compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
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- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACCCCA TCCCATCCAA TAGTCCCAT CTCTCTCAG CTCTCTCTGT AGTTTCTCTT	60
CCTCCGCCTG CCTTTTAACT TAGTGTTTCC CAGGACAGAG GTGACTCAGT TGTATCCAGA	120
CCGCTCTGTG ACTGAACACC CACTTCTTTT TCCTTTTCCA ATAAATATAT GTAACATACA	180
TGTCAACTAG GAACAAAACA GTATCTCAGG AATCCACCAT CCAGTTAAAA ATGGACCCTT	240

ACCCTTACCG TGCCCTGCA GAGACCCCAA TACAGCGCAT TTCCCTCATF CTTTGCTTT	300
TCTCAAGTTT TACCACGGCC TCTTTGGCCC TCGAG	335

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCC AAAGAGGCCG TTGACCATTG ATAGAACACA GGCATACACA GGAAGATACA	60
TTCACAGAAG AGCTTCCTGC ACAAAGTAAG CCACCAGCGC AACATGACAG TGAAGACCCCT	120
GCATGGCCCA GCCATGGTCA AGTACTTGCT GCTGTCGATA TTGGGGCTTG CCTTTCTGAG	180
TGAGGCGGCA GCTCGGAAAA TCCCCAAAGT AGGACATACT TTTTCCAAA AGCCTGAGAG	240
TTGCCCCCCT GTGCCAGGAG GTAGTATGAA GCTTGACATT GGCATCATCA ATGAAAACCA	300
GCGCGTTTCC ATGTCACGTA ACATCGAGAG CCGCTCCACC TCCCCCTGGA ATTACACTGT	360
CACTTGGGAC CCCAACCGGT ACCCCTCGGA AGTTGTACAG GCCCAGTGTA GGAACCTGGG	420
CTGCATCAAT GCTCAAGGAA AGGAAGACAT CTCCATGAAT TCCGTTCCCA TCCAGCAAGA	480
GACCCTGTCG ACGGCCTCTT TGGCCCTCGA GACA	514

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCGACCCTC CACCTGCAAA TCCACTGTCC ATACCCTTGG ATTGGTTGAA GAGCCTTTGG	60
TCATACTGAA CTTCAATTGGA AGTCCGAGGA TTAGGAACAC CGAGAGCAAT AACTTCACTG	120
ATATCCCGAT TTTCAATTCT CTGAAGTTTC GACCTCTTAT CAGGAGCTGC CCTGGAAAGA	180
TTCCGGTCAT GCTGTCTCTC TTTTCGCCTG TCATGCCGGA TTTTCATCCCT CTCACGTGCC	240
TCCCCATCCT CTTTTTCCAC ATGAGTTTTC ATCCAGCTC TTCTCTCCCT GGCTTTCTGG	300
GCCATTTCTC TAAGTTTCTC TNCANGTNTN NCCTTTTCTT TCTGAGCCAT TTTTCTCTCT	360
ACTTGGGGCGT CGACGGCCTC TGGGGCCCTC GAG	393

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCGACCAGG CATAACAGG AAGATACATT CACAGAAAGA GCTTCCTGCA CAAAGTAAGC	60
CACCAGCGCA ACATGACAGT GAAGACCCTG CATGGCCAG CCATGGTCAA GTACTTGCTG	120

CTGTCGATAT TGGGGCTTGC CTTTCTGAGT GAGGCGGCAG CTCGGAAAAT CCCCCAAGTA	180
GGACATACTT TTTTCCAAAA GCCTGAGAGT TGCCCGCCTG TGCCAGGAGG TAGTATGAAG	240
CTTGACATTG GCATCATCAA TGAACCAG CGCGTTTCCA TGTCACGTAA CATCGAGAGC	300
CGCTCCACCT CCCCCTGGAA TTACACTGTC ACTTGGGACC CCAACCGGTA CCCCTCGGAA	360
GTTGTACAGG CCCAGTGTAG GAACTTGGGC TGCATCAATG CTCAAGGAAA GGAAGACATC	420
TCCATGAATT CCGTTCCCAT CCAGCAAGAG ACCCTGGTCG TCCGGAGGAA GCACCAAGGC	480
TGCTCTGTTT CTTTCCAGTT GGAGAAGGTG CTGGTGACTG TTGGCTGCAC CTGCGTCACG	540
TCAACGGCCT CTTTGGCCCT CGAG	564

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCGACCTTC AGTTGCCTCA GACCCAGTA ATACAACGGT CACCACCATG AAACCTACAG	60
CGGCATCTAA TACAACAACA CCAGGGATGG TCTCAACAAA TATGACTTCT ACCACCTTAA	120
AGTCTACACC CAAAACAACA AGTGTTTCAC AGAACACATC TCAGATATCA ACATCCACAA	180
TGACCGTAAC CCACAATAGT TCAGTGACAT CTGTGCTTC ATCAGTAACA ATCACAACAA	240
CTATGCATTG TGAAGCAAAG AAAGGATCAA AATTGATAC TGGGAGCTTT GTTGGTGGTA	300
TTGTATTAAAC GCTGGGAGTT TTATCTATTG TGTCACGGC CTCTTTGGCC CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTA CTGCTGC ACGGACTCTG GAACCATGAA CATATTTGAT CGAAAGATCA ACTTTGATGC	60
GCTTTTAAAA TTTTCTCATA TAACCCCGTC AACGCAGCAG CACCTGAAGA AGGTCTATGC	120
AAGTTTGGCC CTTTGTATGT TTGCGGCGGC TGCAGGGGCC TATGTCCATA TGGTCACTCA	180
TTTCATTGAG GCTGGCCTGC TGTCTGCCTT GGGCTCCCTG ATATTGATGA TTTGGCTGAT	240
GGCAACACCT CATAGCCATG AAAGTGAACA GAAAAGACTG GGA CTCTCTG CTGGATTGTC	300
ATTCCTTACA GGAGTTGGCC TGGGCCCTGC CTTGGAGTTT TGTATTGCTG TCAACCCAG	360
CATCCTTCCC ACTGCTTTCA TGGGCACGGC AATGATCTTT ACCTGCTTCA CCCTCAGTGC	420
ACTCTATGCC AGGCGCCGCG GCTACCTCTT TCTGGGAGGT ATCTTGATGT CAGCCCTGAG	480
CTTGTTGCTT TTGTCGACGG CCTCTTGGC CCTCGAGACA	520

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTCGACGTAC	CACCAGCAAC	CATCAATCCC	GTCTCCTCCT	GCCTCCTCTC	CTGCAATCCA	60
CCCCGCCACG	ACTATCGCCA	TGGCAGCCCT	GATCGCAGAG	AACTTCCGCT	TCCTGTCACT	120
TTTCTTCAAG	AGCAAGGATG	TGATGATTTT	CAACGGCCTG	GTGGCACTGG	GCACGGTGGG	180
CAGCCAGGAG	CTGTCTCTCT	TGGTGGCCTT	CCACTGCCCC	TGCTCGCCGG	CCCGGAACATA	240
CCTGTACGGG	CTGGCGGCCA	TCGGCGTGCC	CGCCCTGGTG	CTCTTCATCA	TTGGCATCAT	300
CCTCAACAAC	CACACCTGGA	ACCTCGTGGG	CGAGTGCCAG	CACCGGAGGA	CCAAGAACTG	360
CTCCGCCGCC	CCCACCTTCC	TCCTTCTAAG	CTCCATCCTG	GGACGTGCCG	CTGTGGCCCC	420
TGTCACCTGG	TCTGTCTCT	CCCTGCTGCG	TGGTGAGGCT	TATGTCTGTG	CTCTCAGTGA	480
GTTCTGTGGAC	CCTTCCTCAC	TCACGGCCTC	TTTGGCCCTC	GAGACA		526

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCAMCTGTG	CAGCGGAGTT	TGACTTTATG	GAAAAAGAGA	CTCCACTGAG	ATACACAAAG	60
ACATTATTGC	TTCCAGTTGT	TCTTGTAGTG	TTTGTGCTA	TTGTTAGAAA	GATTATTAGT	120
GATATGTGGG	GTGTCTTAGC	TAAACAACAG	ACACATGTAA	GAAAACACCA	GTTTGATCAT	180
GGAGAGCTGG	TTTACCATGC	ATTGCAATTG	TAGCATATA	CAGCCCTTGG	TATTTTAATT	240
ATGAGACTAA	AACTCTTCTT	GACACCATAC	ATGTGTGTTA	TGGCATCACT	GATCTGCTCA	300
AGACAGCTAT	TTGGATGGCT	CTTTTGCAAA	GTACATCCTG	GTGCTATTGT	GTTTGTATA	360
TTAGCAGCAA	TGTAATACA	AGGTTGAGCA	AATCTGCAAA	CCCAGTGGA	GTCGACGGCC	420
TCTTTGGCCC	TCGAGACA					438

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCGACCCTA	CACCATGTTT	TTCTCCACGT	TCTACCACGC	CTGCGACCAG	CCCGGGGAGG	60
CGGTGCTGTG	CATCCTCAGC	TACGACACGC	TGCAGTACTG	CGACTTCTTG	GGCTCCGGGG	120
CGGCCATCTG	GGTCACCATC	CTGTGCATGG	CACGGCTCAA	GACAGCCCTG	AAATACGTGC	180
TGTTTCTTCT	GGGTACACTG	GTCATCGCCA	TGTCCTTGCA	GCTGGACCGC	AGGGGCATGT	240
GGAACATGCT	GGGGCCCTGC	CTCTTTGCCT	TCGTGATCAT	GGCCTCCATG	TGGGCTTACC	300
GCTGCGGGCA	CCGGCGCCAG	TGCTACCCCA	CCTCGTGGCA	GCGCTGGGCC	TTCTACCTCC	360
TGCCCCGCGT	CTCTACGGCC	TCTTTGGCCC	TCGAG			395

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTCGACAGAM	WNCAACCCTC	AGACGCCACA	TCCCCTKACA	AGCTGMCAGG	CAGGTTCTCT	60
TCCTCTCACA	TACTGACCCA	CGGKTCCACC	CTCTCTCCCC	TGGAAAGGAC	ACCATGAGCA	120
CTGAAAGCAT	GATCCGGRAC	GTGGAGCTGK	CCGAGGAGGN	GYTCCCCAAG	AAGACAGGGG	180
GGRCCCAGGG	CTCCAGGCGG	GGGTTTGTTT	CTCAGWCTCT	TCTCCTTCCT	GATCGNGGGA	240
GGGGGCACCA	CGCTCTTCTG	TCTGCTGGAC	TTTGGAGTGA	TCGGNCCCCA	GAGGGAAGGA	300
GTCCCCCAGG	GGAACCTCTC	T				321

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 532 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTCGACGGCC	GAGAWGGACA	TGAAGCAATA	TCAAGGCTCC	GGCGGCGTCG	CCATGGATGT	60
GGNACGGAGT	CGCTTCCCCT	ACTGCGTGGT	GTGGACGCCC	ATCCCGGTGN	TCACGTGGTT	120
TTTCCCCATC	ATCGGCCACA	TGGGCATCTG	CACATCCACA	GGAGTCATTC	GGGACTTCGC	180
GGGCCCCCTAC	TTTGTCTCAG	AGGACAACAT	GGCCTTTGGA	AAGCCTGCCA	AGTACTGGAA	240
GTTGGACCCT	GCTCAGGTCT	ATGCTAGCGG	GCCCAACGCA	TGGGACACGG	CTGTGCACGA	300
CGCCTCTGAG	GAGWACAAGC	ACCGCATGCA	CAATCTCTGC	TGTGACAACT	GCCACTCGCA	360
CGTGGCATCG	CCCCTGAATC	TGATGCGCTA	CAACAACAGC	ACCAACTGGA	ATATGGTGAC	420
GCTCTGCTTC	TTCTGCTGTC	TCTACGGGAA	GTACGTCAGC	GTTGGGGCCT	TCCTGAAGAC	480
CTGGCTGCCC	TTCATCCTTC	TCCTGTCGAC	GGCCTCTTTG	GCCCTCGAGA	CA	532

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGTACACCA	AGATGATGAC	CAAGAAGCCG	GGCATGTTCT	TCAACCCCGA	GGAGTCGGAG	60
CTGGACCTGA	CCTACGGNAA	CAGATACAAN	AACGTGAAGC	TCCCTGACGN	CTACGAGCGC	120
CTCATCCTGG	ACGTCTTCTT	TGGGAGGCAG	ATGNACTTCG	TGCGCAGGGA	CGANCTCCNT	180
GAGGNCTGGC	GTATTTTTCA	CCCCACTGNT	TACCANATT	GAGCTNGAGA	AGGCCAAGCC	240
TCCAGGAACA	CATGTGGGGT	CATTACCAAA	CAGGGTCCAT	CCACATGATG	GTGAACATCA	300
ANCTTTGGGC	GGACAANGAT	TGCTGGGAAT	GGGAATCCTG	TTCCTGGGG	AGCTCTGGGA	360
GTTCTTGAGC	TTTGCTGAAA	GGTACCCTGC	CATCATCTAT	AACATCCTGC	TCTTTGGGCT	420
GACCAATGCC	CTGGGTCAGA	GCWTCATCTT	TATGACGATT	GTGTATCTTG	GTCCCCTGAC	480
CTGCTCCATC	ATCACTACAA	CTCGAAAGTT	CTTCACAAAW	KTGCCCCGCTG	TGATCCTCTT	540
CGCCAATCCC	ATGTCGACGG	CCTCTTTGGC	CCTCGAGACA			580

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

GTCGACACTA CTTATGCGGC TACTTTGTCC AGGGCACAAA ATGCCGTGGC AGTATCTAAC      60
TAAACCCCCA CAAAACTGCT TAATAACAGT TTKGRATGTG AGAAATTAG ATAATTTAAA      120
TATAAGGTGC AGGTTTAAAT TCTGAGTTT CTTCTTTTCT ATTTTATTA AAAAGAAAAT      180
AATTTTCAGA TTTAATTGAA TTGAAAAAAA CAATACTTCC CACCAGAAAT ATATATCCTG      240
AAAATTGTAT TTTTGTATA TAAACAACTT TTAAGAAAGA TCATTATCCT TTTCTCTACC      300
TAAATATGAG GAGTCTTAGC ATAATGACAA ATATTATAA TTTTCAATT AATGGTACTT      360
GCTGGATCCA CACTAACATC TTGCTAATA ATCTCATTGT TTCTTCGTCA ACGGCCTCTT      420
TGGCCCTCGA GACA                                     434
  
```

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 523 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

GTGGACGTTT TTTTTTCTT TTTCTTTTTT TTAAGAAAAA CCCATTTTTT TCCTTAAGGA      60
CTTACTAGCC AAAATTTCTT AAACCTCGAG GACTCTACTA GCCATGGCCG AGCCATTCTT      120
GTCAGAAATAT CAACACCAGC CTCAAACAGT CAACTGTACA GGTGCTGCTG CTGTCCAGGA      180
AGAGCTGAAC CCTGAGCGCC CCCCAGGCGC GGAGGAGCGG GTGCCCGAGG AGGACAGTAG      240
GTGGCAATCG AGAGCGTTCC CCCAGTTGGG TGGCCGTCCG GGGCCCGAGG GGGGAAGGGAG      300
CCTGGAATCC CAACCACTC CCTTGCAGAC CCAGGCCTGT CCAGAATCTA GCTGCCTGAG      360
AGAGGGCGAG AAGGGCCAGA ATGGGGACGA CTCGTCCGCT GGCGGCGACT TYCCGCCGCC      420
GGCAGAAAGTG GAACCGACGC CCGAGGCCGA GCTGCTCGCC CAGCCTTGTC ATGACTCCGA      480
GGCCAGTAAG ATGGGGTCGA CGGCCTCTTT GGCCCTCGAG ACA                          523
  
```

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

GTCGACCCTC ANTGTTCTGG AACTGGTCTT GGAAGGGATN GTTTATNCTG AGTACACCTG      60
GGAAGTATTT GGGTACTGTC ANGAGCTGGA GTTGNCTNG NATTACCNTC TTCTGCCCNA      120
TCTGGTGGTA GGGGTAAACC NG                                     142
  
```

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 534 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

GTCCACCCGG GCCGCCCTC GCCGCCGGG CTCTTCGCGG GCTGCTCTTT GTCTCCCCGA      60
CCTCGATCCC TGGCTCTCCG GCGGCGTGCG GGCTCGTCTG AGGCTTCCCG CATCTCCCCG      120
CTGGAAC TCC TGCCTCCCG GGGTTAGAGG AGGTTTCGTT CGAGGGCTGG AAGCGGGAAG      180
GCGGGGCGGA AGGACTGGGC TCATCGCCTC CTGATTAAC TGTGTCTTT ACTTAAAATG      240
ACTTTTCCCC CACTTTGTCA AACTTGAGAA CTGTSTTGTG TGTGTGTGTT TCCTTGAGTC      300
TCTAGCTTCA AAATTAAGAG TAGGCGCTAC CGCTGCGATT GTGGGCAGTT GTGTGGTTGG      360
CGGCTGCGTT TGGAGCTCTG AGTTGAAAAG ATGTACGTGA ATGTATGGTT TAGATTTTGT      420
TCTTTTTTTT GCGATTGTC TATTGGGAGT ACTTTTCCTT TCGGAAATGG GCGAATTTGG      480
TTTTCTTTT GTTCATTGAG AACTGGGTCG ACGGCCTCTT TGGCCCTCGA GACA          534
  
```

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 558 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

GTTCMCGAAG GGAAGAAGAA GATGAACAAG AACAATGCCA AGGCTCTGAG CACCTTGCGT      60
CAGAAGATCC GAAAATACAA CCGTGATTTC GAGTCCCATA TCACAAGCTA CAAGCAGAAC      120
CCCAGCAGT CTGCGGATGA AGATGCTGAG AAAAGTGAGG AGGATTCAGA AGGCTCTTCA      180
GATGTGGATG AGGATGAGGA CGGAGTCAGT GCTGCAACTT TCTTGAAGAA GAAATCAGAA      240
GCTCCTTCTG GGGAGAGTCG CAAATTCCCTC MAAAAGATGG ATGATGAAGA TGAGGACTCA      300
GAAGATTCCG TAGATGATGA AGACTGGGAC WCAGGTTCCA CATCTCCGA CTCCGACTCA      360
GAGGAGGAAG AAGGGAACA AACCGCGCTG GCCTCAAGAT TTCTTAAAAA GGCACCCACC      420
ACAGATGAGG ACAAGAAGGC AGCCGAGAAG AACCGGGAGG ACAAAGCTAA GAAGAAGCAC      480
GACAGGAAAT CCAAGCGCCT GGATGAGGAG GAGGAGGACA ATGAAGGCGG GGTACAGGCC      540
TCTTTGGCCC TCGAGACA          558
  
```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 465 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

GTTGACGGCC AGCTTGCTGT CTAAC TTTTC ACATCGGAGA AGCTCCTTGG CCTGGGAGGA      60
CTTCTCCGTG CCTTCCCCCT TCCCAGAGAT GCCCCTGTG AGGGAGTGGC AGAGACCATC      120
CTGGAGGGTG CCAGGAGCGG GGGCCCGTCT GAAGTCCCCG CCACCCTGGC GGTGCTCCGC      180
AGGCACCGGG CCATCCGACA TCGCACCTC GCTGGCGCGC ACGCTGGCCT GCTTGTGAAG      240
  
```

AGCATCCTTC AGCAGGCTGC CCAGCGGTGG CGCCTCCTGC ATAGACGCTT TGTTTTCAAA	300
AGTACTTGAC CTTTCCACAG CCTTCGGATA GACTTTCTTC TCTCTCTCTT CCAGCTTAAA	360
CAGAGCAAAG TTTTCCAAAT CACTCCCGGG TCCATGGGAT TTCTGGTGGG ATTCCTGTTT	420
CTCTGGGAAG CCGTCTGGTC GACGGCCTCT TTGGCCCTCG AGACA	465

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 694 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GNNNTCGTTG TTCCAGAACT TGATGAGGGG ATCTCGGAAC AACACNGAAA CTTTTCCCTC	60
CCTCANTNAC GCACCNCGAC TCTCTATTGA GCCAACGGNA ANNCGGCCCT TCCCTCCAAG	120
TAACCTTGN A TTTGAAAATA AAAAAAAAAAG NTTGCTGTCC TTGCTATCCA AGAATAAATA	180
GACCTNCAAN TATTAATCTT TTGTTTCCCT CGTCATTGTT CTCGTTCCCT TTCTNCCTTG	240
TTTCTTTTTC TGCACAATAT ATCAAGCNAT ACCAAGCATA CAATCAAACCT CCAAGCTCGG	300
AATTCGGCCA NAGAGACCGT CGACGGAAGA AATTGNCTGG AAACCTGTTC ATGGTGATAT	360
ATACCGTCCN CCAAGAAAAG GGATGCTGCT ATCAGTCTTT CTAGGATCCG GGACACAGAT	420
ATTAATTATG ACCTTTGTGA CTCTATTTT CGCTTGCCTG GGAGTTTGT CACCTGCCAN	480
CCGAGGAGCG CTGATGACGT GTGCTGTGGT CCTGTGGGTG CTGCTGGGCA CCCCTGCAGG	540
CTATGTTGCT GCCAGATTCT ATAAGTCCTT TGGAGGTGAG AAGTGAAAA CAAATGTTT	600
ATTAACATCA TTTCTTGTG CTGGGATTGT ATTTGCTGAC TTCTTTATAA TGAATCTGAT	660
CCTCTGGTCA ACGGCCTCTT TGGCCCTCGA GACA	694

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGACTCGTCT CAGACCAGTT GCAGCCTTCT CAACCCAAAC GCCGACCAAG GAAAACTCA	60
CTACCATGAG AATTGCAGTG ANTTGCTTTT GCCTCCTAGG CATCACCTGT GCATACCAG	120
NTAAACAGGC TGATTCTGGA AGTTCTGAGG AAAAGCAGCT TTACAACAAA TACCAGATG	180
CTGTGNCCAC ATGGCTAAAC CCTGACCCAT CTCAGAAACA GAATCTCCTA GCCCCACAGA	240
CCCTTCCAAG TAAGTCCANC GAAAGCCATG ACCACATGGA TGATATGGAT GATGAAGATG	300
ATGATGACCA TGTGGACAGC CAGGACTCCA TTGACTCGAG CGACTCTGAT GATGTAGATG	360
ACACTGATGA TTCTCACCAG TCTGATGAGC CTCACCATTC TGATGAATCT GATGAAGTGG	420
TCACTGATTT TCCACGGAC CTGCCGTCGA CGGCCTCTT GGCCCTCGAG ACA	473

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

AGAAGCTGTG ATCTTCAAGA CCATTGTGTC CAAGGAGATC TGTCTGATCC CAAGCAGAAG      60
TGGGTTCAGG ATTCCATGGA CCACCTGGAC AAGCAACCCA AAACCTCCGAA GACGTGAACA      120
CTCACTCCAC AACCCAAGAA TCTGCAGCTA ACTTATTTTC CCCTAGCTTT CCCCAGACGT      180
CGACGCCTCT TTGCCCTCGA GACA                                         204

```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

GTCCACACAC GCCGACCACG GAAAACACAC TACCATGAGA ATTGCAGTGA TTTGCTTTTG      60
CCTCCTAGGC ATCACCTGTG CCATACCACT TAAACAGGCT GATTCTGGAA GTTCTGAGGA      120
AAAGCAGCTT TACAACAAAT ACCCAGATGC TGTGGCCACA TGGCTAAACC CTGACCCATC      180
TCAGAAGCAG AATCTCCTAG CCCCACAGAA TGCTGTGTCC TCTGAAGAAA CCAATGACTT      240
TAAACAAGAG ACCCTTCCAA GTAAGTCCAA CGAAAGCCAT GACCACATGG ATGATATGGA      300
TGATGAAGAT GATGACGACC ATGTGGACAG CCAGGACTCC ATTGACTCGA ACGACTCTGA      360
TGATGTAGAT GACACTGATG ATTCTCACCA GTCTGATGAG TCTCACCATT CTGATGAATC      420
TGATGAACTG GTCAC TGATT TTCCGTCGAC GGCTCTTTG GCCTCGAGA CA              472

```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

GTCGACTGAA AATTAACCCT CAGACGCCAC ATCCCCTGAC AAGATGCCAG GCAGGTTCTC      60
TTCCTCTCAC ATACTGACCC ACGGGTCCAC CCTCTCTCCC CTGGAAAGGA CACCATGAGC      120
ACTGAAAGCA TGATCCGGA CGTGAGCTG GCCGAGGAGG NNTTNNCCAA GAAGACAGGG      180
GGGGCCCAGG GGTCCAGGNG GNGCTTGTTT CTCAGACTCT TCTCCTTCCT GATCGTGGA      240
GGNGNCACCA CGCTCTTCTG NCTGNTGNAC TTTGGAGTGG ATCCGGGCCC CAGAGGGAAG      300
AGTTCCCCCA GGGGACTCTT CTCTAATCNA GNCCTCTTGG                        340

```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTCGACGCGC GCCGGTAAAA ATGGCGAAAT GGGGGTAGGC GGCGCTGGAC CTGAAGAGAT	60
GGGGCGCGCA GGTGGGGCGG TTGTCAGAGC CCCCTGACGT GGGCGCCGGG CTTTATCGG	120
CGATTTGATC TGGCGACCTC GGGCCGCGC CTAAGAGGTC AGACTGCGGA GCCTGCGGGT	180
CGCCAGCGGC CCCGCCGAGT GCCGGAGGCA ATGGATGAAC AGAGCGTGGA GCGCTGKCTG	240
WCAGAGCAGA GAGCTCAATG TCCTCATTCC CGTGCTCCAC TCCAGCTACG AGAACTAGTA	300
AATTGTCGTT GGGCAGAAGA AGTAACACAA CAGCTTGATA CTCTCAACT CTGCAGTCTC	360
ACCAAACATG AAGAAAATGA AAAGGACAAA TGTGAAAATC ACCATGAAAA ACTTAGTGTA	420
TTTGTCTGGA CTTGTAAGAA GTGTATCTAC CATCAGTGTG CACTTTGGGT CGACGGCCTC	480
TTTGGCCCTC GAGACA	496

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGACACATAG ACCAACCGGG GAGATATGTT TGAATNTGAT GAAGATGAGA TGTTCTATGT	60
GGATCTGNAC AAGAAGGAGA CCTCTGTCTAT CTGGAGGAGA NTGNCCAACC CTTTCTCTT	120
GAGNCTCAGG GNGGGCTGTC TAACATTGCT ATANTGAACA ACAACNTGAA TACCTTGATC	180
CAGCGTTCCA ACCACACTCA GNCCACCAAC GATCCCCCTG AGGTGACCGT GTTCCCAAG	240
GTACGGCCT CTTTGCCCT CGAGACA	267

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCGACCTTG AAGATGTTTT CTAAAGAATC AAAAATGCTA CAAAGAAGTA TATCATTTTC	60
AAATATGGCT TTATCGTCTT GTTTACTTTT ACCAGGAGAT GCCACTGTCA TAACCTCTTC	120
ATGGGATAAT AATGTCTATT TTTATTCCAT AGCATTGGA AGACGCCAGG ACACGTTAAT	180
GGGACATGAT GATGCTGTTA GTAAGATCTG TTGGCATGAC AACAGGCTAT ATTCTGCATC	240
GTGGGACTCT ACAGTGAAGG TGTGGTCTGG TGTTCTGCA GAGATGCCAG GCACCAAAG	300
ACACCACTTT GACTTGCTGG CCGAGCTGGA ACATGATGTC AGTGTAGATA CAATCAGTTT	360
AAATGCTGCA AGCACACTGT TAGTTTCCGG CACCAAAGAA GGCACAGTGA ATATTGGGA	420
CCTCACAACG GCCTCTTTGG CCCTCGAGAC A	451

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GTTGACGCAA GTTGCTGGGC TGGTGGGGGC CTGTCAAGTG AGGCCTGGTG GAGAAAGGTT	60
GAATTTGGAG GGCCAGGAAC AAGCTGGGAT GCAGGGGAGG CTTTCTAAAC TCTACAGTGC	120
TTCTAGAGAT GACGAGGAGG TAGGGAGTAG AAGAGAGCCG GACAGATTAG GGAGCTCCCA	180
GGGTGAGCTT GTGGGCAGSC CTSCAGAGGA GAAGAGGCTC TTCCCTAGGA GCTCAGAGGG	240
ACTTGTCTG GAAGACTGAT GGGAGATGTA TGCAGCTGTT TAGAGGCTGC TTTGGAGAAC	300
AAATGAACAT GGTTCGTGTT GTGCAAGCAG TTACTGTGGT TCTTTTGGCT CATATATCTT	360
CCAATAAAGA CATTGAGCGA GGAGAGTTGA TACCGTCATG TTTTGGAGC TTAAGCACAG	420
ACTGGCAGGT CGACGGCCTC TTTGGCCCTC GAGACA	456

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCGACAGAA TTCACAACAT CCCAAGATTC CACCTCNCAA GATGTTTTCT AAAGNAATCA	60
AAAATGCTAC AAAGAAGTAT ATCATTTTCA AATATGGCTT TATCGTCTTG TTTACTTTTA	120
CCAGGAGATG CCACTGTTCAT AACTTCTTCA TGGGATAATA ATGCTATTTT TTATTCCATA	180
GCATTTGGAA GACGCCAGGA CACGTTAATG GGACATGATG ATGCTGTTAG TAAGGATCTG	240
TTGGCATGAC AACAGGCTAT ATTCTGCATC GTGGGACTCT ACAGTGAAGG TCGGCTCTGG	300
TGTTCCCTGC AGAGATGCCA GGCACCAAAA GACACCACTT TGGCTTGNTG GCCGAGCTGG	360
ACATGATGTC AGNGTNGGTA CAATCAAGNT TANNA	395

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTGGNCCGAG ATAGAGGAGG CTCCCTCCA AGAGGACCCC GGNGTTCCCG AGGGAACCCC	60
TCTNGAGGAG GAAACGTCCA GCACCGAGCT GGAGACTGGC AGTGTCCCAA TCCGGGTTGT	120
GGAAACCAGA ACTTCCCCTG GAGAACAGAG TGCAACCAGT GTAAGGCCCC AAAGMCTGAA	180
GGCTTCCTCC CGCCACCCTT TCCGCCCCG GGTGGTGATC GTGRCAGAGR TGGCCCTGST	240
GGCATAACGGG GAGGAAGAGR TGGCCTCATG GATCGTGGTG GTCCCGGTGG AATGTTTCTG	300
GRTGGYCGTK GTGGAGACAG AGRTGKCTTC CGTKGTGGCC GGGGCATGGA CCGAGGTGKC	360
TTTGGTGGAG GAAGACNAGG TGTCCCTGGG GGCCCCCTG NTCCTTTGAT GGAACAGATG	420
GGAGGAAGAA GAGGAGGACG TGGGTCGACG NCCTCTTTGT CCCTCGAGAC A	471

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTCGACCGTC	TACGCCTACA	CCATGTTCTT	CTCCACGTTT	TACCACGCCT	GCGACCAGCC	60
CGGGGAGGCG	GTGCTGTGCA	TCCTCAGCTA	CGACACGCTG	CAGTACTGCG	ACTTCTTGCG	120
ATCCGGGGCG	GCCATCTGGG	TCACCATCCT	GTGCATGGCA	CGGCTCAAGA	CAGTCCTGAA	180
ATACGTGCTG	TTTCTTCTGG	GTACACTGGT	CATCGCCATG	TCCTTGCCAGC	TGGACCGCAG	240
GGGCATGTGG	AACATGCTGG	GGCCCTGCCT	CTTTGCCTTC	GTGATCATGG	CCTCCATGTG	300
GGCTTACCGC	TGCGGGCACC	GGCGCCAGTG	CTACCCCAACC	TCGTGGCAGC	GCTGGGCCTT	360
CTACCTCCTG	CCCGGCGTCT	CTACGGCCTC	TTTGGCCCTC	GAGACA		406

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GTCGCCCAGC	AAGTGAGCAG	ATCCTCCGAG	GCACCAGGGA	ACTCCAGCCC	ATGCCATGGC	60
GGATTCTGAG	CGCCTCTCGG	CTCCTGGCTG	CTGGGCGCGC	TGCACCAACT	TCTCGCGCAC	120
TCGAAAGGGA	ATCCTCCTGT	TTGNTGAGAT	TATATTATGC	CTGGTGATCC	TGATCTGCTT	180
CAGTGNCTCC	ACACCAGGCT	ACTCCTCCCT	GTCGGTGAYT	GAGATGATCC	YTSCTCSCTA	240
TCTTTCCTYT	GTTGTCTACA	TGTGTGACCT	GCACCACCAA	GATACCATTG	ATCAACTGSS	300
CCTGGAGTGA	TTTCTTCCGA	ACCCTCATAG	GGGSAATCCT	CTACCTGATC	AMCTCCATTG	360
TKGTCTCKGT	TGAGAGAGGA	AACCACCCCN	TNAATCGTTC	GTAGGGGTAC	TGGGCCTAAT	420
CGCTACGGCC	TCTTTGGCCC	TCGAGACA				448

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTNCAATCNC	CGATCCCCAT	CACGAATGGG	GGGCACCGGG	TTACCCCCCC	CCTCCCGCCG	60
TAGGGTAGGC	ACACNCTGAG	CCAGTCAGTG	TATCGCGCGT	GCATCCCCGG	ACATCTAAGG	120
GCATCACAGA	CCTGTTNTTG	NTCAATCTCG	GGTGGNTGNN	CGCCACTTGT	CNCTCTAAGA	180
ANATGGGGGA	CGCCGNCCGC	TCGGGGGTNG	CGTAACTAGN	TAGNATNCCA	GAGTCTCGTT	240
CGTTATCGGA	AGTAACCAGA	CANATCGCTC	CNCCAATAA	GANNGGCCAT	NCACCACCAC	300
CCACGGAATC	GAGANAGAGC	TATCAATCTG	TTGTAGGACA	TAACCCGGCT	TCTTGGTTCAT	360
CATCNTGGTG	TACNCGNCCT	CTTGNCCCT	CGAGACA			397

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TCCTGCCTGC TGGGCCGCCT TNCACCCAAC TTCTCGCGCA CTCGAAAGGG AATCCTCCTG	60
TTTGCTGAGA TAAATANTAT NCCTGGTGAT CCTGATCTGC TTCAGTGCCT CCACACCAGA	120
CNACTCCTCC CTGTCGGTGA TTGAGATGAT CCTTGCTGCT ATTTTCTTTG TTGTCTACAT	180
GTGTGACCTG CACACCAAGA TACCATTCAT CAACTGGCCC TGGAGTGATT TCTTCCGAAC	240
CCTCATAGCG GCAATCCTCT ACCTGATCAC CNCCGTTGTT GTCCTTGTTG AGAGAGGAAA	300
CCACTCCTAC AATCGTCGCA GGGGTACTGG GCCTAATCGC TACGGCCTCT TTGGCCCTCG	360
AGACA	365

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTCGACGACA CGCTGTCTTC ACTACCTGAT TGCCGAGAAG ATCCCACTG TCTACACTAC	60
CTGCCTGGCC AGTAGATCCA CGGTATCTAC ACTACCTCCC TGGCCAGCAG ATTCACCCAG	120
TCTACACTAA CCGTTGTCC AGCAGGTCCA CCCTGTCTAC ACTACGTGCC TGCCAGCAGA	180
TCCAAGCTGT CTACACTCCC TGCCTGGCCA GTAGATCCAT GCTATCTCCA CTACCTGCCT	240
ATCCAAGTGA TCCACCCTCT CTTTACTACC TTCCTGTCCG GCAGATTGAC CCTCTCTACT	300
CTACCTGCCT GGCCAGCAGA TCCACGCTAT CTACACTACC TGACTTACCA GATCCACCCCT	360
GTCTACACTA CATGCTTGTC CAGCAGGTCC ACCCTGTCTA CACTACCTGC CTCTCCAGAA	420
GATCCACGTC AACGGCCTCT TTGGCCCTCG AGACA	455

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGANTTNGG CCCAAAGAGC CCGTTTGAGT NAACCAAGA AGTCAAGATT GGCCCAAGT	60
TCCAGANATG TTTTGAAGAC CTGGAGAACT GTTACAGTGN AAATGAAGAA GACAGTTCCT	120
CCATTGATCA TCTGTCTCTG AATCAGAAAT CCTTCTATCA TGTAAGCTAT GGCCCACTCC	180
ATGAAGGCTG CATGGATCAA TCTGTGTCTC TGAGNATCTC TGAAACCTCT AAAACATCCA	240
AGCTTACCTT CAAGGAGAGC ATGGTGGTAG TANCANCAA CGGGAAGGTT CTGAAGAAGA	300
GACGGTTGAG TTTAANCCAA TCCATCACTG ATGATGACCT GGAGGCCATC GCCAATGACT	360
CAGAGGAAGA AATCATCAAG CCTAGGTCAT CACCTTTTAG CTCCCCGAGC AATGTGAAAT	420
ACAACTTAT GAGGATCATC AAATACGAAT TCATCCTGAA TGACGCCCTC AATCAAAGGT	480
CGACGGCCTC TTTGGCCCTC GAGACA	506

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGTAACGCN GTTNTCCTNA GGCGAGCTCA GGGAGNACAA GAAACCCTCC CGTGGAGCAA	60
GAANGCCACA AGCTCNCTTG ATCTTGATTA TCAGGACGAA AACAGACCGT GAAAGCGGGG	120
CCTCAGCATC CTTCTGACCT NNTGGGTNTT AAGCAGGAGG TGTCAGAAAA GTTNCCACAG	180
GGATAACTGN CTTGTGNCGN CCAAGCGNTC ATAGCGACGT CGCTTTTGA TCCTTCGATG	240
TCGGCTCTTC CTATCATTGT GAAGCAGAAT TCACCAAGCG TTGGATTGTT CACCCACTAA	300
TAGGGAACGT GAGCTGGGTT TAGACCGTCG TGAGACAGGT TAGTTTTACC CTACTGATGA	360
TGTGTTGTTG CCATGGTAAT CCTGCTCAGT ACGAGAGGAA CCGCAGGTTT AGACATTGG	420
TGTATGTGCT TGGCTGAGGA GCCAATGGTC GACGGCCTCT TTGGCCCTCG AGACA	475

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GTGACCCGA TGGAGGAGGA GGAGGTTGAG ACGTTCGCCT TTCAGGCAGA AATTGCCAG	60
TTGATGTCAT TGATNCATCA ATACTTTCTA CTCGANCAAA GAGATCTTTC TGAGAGAGCT	120
CATTTCAAAT TCATCAGATG CATTGGACNC AATCCGGTAT GAAAGCTTGA CAGATCCAG	180
TAAATTAGAC TCTGGGAAAG AGCTGCATAT TAACCTTATA CCGAACAAN AAGANCGAAC	240
TCTCACTATT GTGGATACTG GAATTGGAAT GACCAAGGCT GACTTGATCA ATAACCTTGG	300
TACTATCGCC AAGTCTGGAC CAAAGCGTTC ATGGAAGCTT TGCAGGCTGG TGCAGATATC	360
TCTATGATTG GCCAGTTCGG TGTGTTTAT TATTCTGCTT ATTTGGGTGC TGAGAAAGTA	420
ACTGTGATCA CCGTCGACGG CCTCTTTGGC CNGCGAGACA	460

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TCAAGCAATA CCCAAGCAAA CAATCNACTC CAANCTCGGA ANTCGNCCNA AGAGACCGTC	60
GACCCCGTGT TCACNATGGT AGNNACGCCG NCTACCATCG ANAGTTGATA GGGCAGACGT	120
TCGNGTGGGT CGTCTCCCC CCGGGGGGCG TGCGATCGCC CCGAGGTAT CTAGAGTCAC	180
CACACCCGCC GCGGCCCNCC CCCCNCNCGN NAAAAAAGA GGGGCTGTCT GGGNTGGTTT	240
TGNTNTGATA AATANACGCA TCCCCCCCC GNNGGGGGNN AGCGCCCGTC GGCATGTATT	300
ANCTCTAGAA TTACCACAGT TATCCAAGTA GGAGAGGAGC GAGCGNCCAN AGGANCCATA	360
NCTGATTAA TGAGCCATTC NCAGTTTCNC TGTTCGNCC GTGCGTACGN AACGACCTCT	420
TTGTNCNTAA AGNCG	435

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

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GTCGACCACA CTGCTGCTCA CGCTCAGCAA CCTCATGTTC CTGGCCCCCA TCGCCGTCTC      60
AGTGCGGCGA TTCTTCTGG TGGAGGCCTC CGTCTACGCC TACACCATGT TCTTCTCCAC      120
GTTCTACCAC GCCTGCGACC AGCCCGGGGA GGCGGTGCTG TGCATCCTCA GCTACGACAC      180
GCTGCAGTAC TCGCACTTCT TGGGCTCCGG GGCGGCCATC TGGGTCACCA TCCTGTGCAT      240
GGCACGGCTC AAGACAGTCC TGAAATACGT GCTGTTCTT CTGGGTACAC TGGTCATCGC      300
CATGTCTTGG CAGCTGGACC GCAGGGGCAT GTGGAACCTG CTGGGGCCCT GCCTCTTTGC      360
CTTCGTGATG ATGGCCTCCA TGTGGGCTTA CCGCTGCGGG CACCGGCGCC AGTGCTACCC      420
CACCTCGTGG CAGCGCTGGG CCTTCTACCT CCGCCCGGC GTCTCTACGG CCTCTTTGGC      480
CCTCGAGACA                                     490

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(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

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CGTCTCAGGC CAGTTNCANC CTTCTCANNC AGAACGGCGN CCCAAGGAAA ANCTCACTAC      60
CATGAAGAAT TGCAGTGATT TGCNTTTGCC TCCTAGGCAT CACCTGTGCC ATACCAGNTA      120
AANCAGGCTG ATTCTGGAAG TTNCTGAGGG AAAAAGCAGC TTTACAACAA ATACCCAGAT      180
GCTGTGGCCA CATGGCTAAA CCCTGANCCA TCTCAGAAGC AGAATCTCCT AGCCCCACAG      240
AATGCTGTGT CCTCTGAAGA AACCAATGAC TTAAACAAG AGACCCAAAC AAGTNAGTCC      300
NACGAAAGCC ATGACCACAT GGATGATATG GATGATGAAG ATGATGATGA CCATGTGGAC      360
AGCCAGGACT CCATTGACTC GNNCGACTCT GATGATGTAG ATGACACTGA TGATTCTCAC      420
CAGTCTGACG AGTCTACCA TTCTGATGAA TCTGATGAAC TGGTCACTGA TTTCCCACG      480
GACCTGCCGT CGACGGCCTC TTTGACCCTC GAGACA                                     516

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(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

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GCCAAGACTC GTCTCAGNCC AGTTGCAGCC TTCTCANCCA AACNCCGACC CAAGGANAAC      60
TCCCCTACCA TGAGAATTGC AGTGATTTGC TTTTGCCTCC TAGGCATCAC CTGTGCCATA      120
CCAGTTAAAC AGGCTGATTC CTGGAAGTTC CTGAGGAAAA GCAGCTTTAC AACAAATACC      180

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CAGATGCTGT	GTCCACATGG	CTAAACCCCTG	ACCCATCTCA	GAAGCAGAAT	CTCCTAGCCC	240
CACAGAATGC	TGTGTCTCT	GAAGAAACCA	ATGACTTTAA	ACAAGAGANN	CANCCAAGTA	300
AGTCCANCGA	AAGCCATGAC	CACATGGATG	ATATGGATGA	TGAAGATGAT	GATGACCATG	360
TGGACAGCCA	GGACTCCATT	GACTCGANCG	ACTCTGATGA	TGTAGATGAC	ACTGATGATT	420
CTCACGAGTC	TGACGAGTCT	CACCATTCTG	ATGAATCTGA	TGAACTGGTC	ACTGATTTTC	480
CCACGGACCT	GCCGTCGACG	GCCTCAATGN	CCCTCGAGAC	G		521

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GCAAGCAANC	AATCCAACCC	AAGNTNGGGA	NTCGNCCNAA	GAGNCCGTTG	ANCAGAAGCC	60
ANTNATGGAT	GANCAGCGCG	ACCTTATCTC	CAACAATGAG	CAACTGNCCA	TNCTGGGNCC	120
GGNCGCCCTG	GGGCNCCGGA	GAGCAAGTGC	ANCCGCGGAG	CCCTGTACAC	AGGCTTTTCC	180
ATCCTGGTGA	CTCTGCTCCT	CGCTGGCCAG	GCCACCACCG	CCTACTTCCT	GTACCAGCAG	240
CAGGNCCGGC	TGGACAAACT	GACAGTCACC	TCCCAGAACC	TGCAGCTGGA	GAACCTGCGC	300
ATGAAGCTTC	CCAAGCCTCC	CAAGCCTGTG	AGCAAGATGC	GCATGNCCAC	CCCGCTGCTG	360
ATGCAGGCGC	TGCCCATGGG	AGCCCTGCCC	CAGGGGCCCA	TGCAGAATGC	CACCAAGTAT	420
GGCAACATGA	CAGAGGACCA	TGTGATGCAC	CTGCTCCAGA	ATGCTGACCC	CCTGAAGGTG	480
TACCCGCCGT	CGACGGCCTC	TTTGGCCCTC	GAGACA			516

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGCTATCCNA	GNATAAAATA	AGACCCTGCA	ANTATTAATC	TINTTTGTTT	CCTCGTCATT	60
GTTCTCGTTC	CCTNTCTTCG	TTGTTTCTNN	TTCTGCACAA	TATNTTCAAG	CTATACCGAG	120
CATACAATCA	AACTCCAAGC	TCGGAATTCG	NCCAAAGAGG	CCGTGCGGCC	GAATTCTCCA	180
CNAGAATAGC	ATTTCTGCTC	ATCTGCATGG	TCGCAGTCAC	GAGCCAGATG	NCCTGNTTIN	240
CCACAGTTGT	AGCAGCATTG	CTCTCGCTCT	CTCTTGGGCT	CCTTGCGATC	CTTGGCAATG	300
TGGCCGCCTC	TACCGCAGTT	ATAGCAGGCA	TCCTCCTGAA	GATCACAATC	CTTGGCAAGA	360
TGACCAGACT	CACCACAGCG	ATAACAAATA	TCTGGAAGAG	ACGAGGAAAC	AAACTGGAAA	420
CCTCTATCCG	AGGTAAACC	ACCTCTGCCA	CGGCTTCTCA	TTCCACGACC	ACGGCCTCTT	480
TGGCCCTCGA	GACA					494

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCTCCANATN	ANCTTTNTTC	CTCTCATTGT	NTCGTCCCTC	CTCCTTGTTT	TTTNTGCCC	60
AAAATCCANC	AAANCCAACA	ACCATCCNCN	CCACCTGGAA	GTNGCCCAAA	GAGGCCGNAC	120
CAAGAAGTGT	CGATTCCTTT	GTNTGNAGGA	GCGACCAGGA	ACATCTACGG	TTGAGAAGAA	180
AGAAAGANTG	CCTTCGTCTG	TGTCTTCCTG	TGTGAANTTT	CCAGACATAG	CCCAGTCGAC	240
CAGCCTTCCC	CACNAGACTG	GAGCGTCTCT	ATTGTATNTG	GGTCCCTGTA	AGAGTAGAAG	300
GGTGAATAATC	CCANTGTGTC	TGAGTNTTGC	GCCNCCACCA	TAAACACCGC	CTTTTCTCTG	360
AATTTCTGTA	TNCAAGAAAN	TGTCAGTCAT	CACACGTGCA	AGGATNTTAA	GACTGNCATG	420
ATCTGGGNCC	GTGTAGGGGN	CAGNTCGGAT	NCATTACCCC	ACGTAATTCA	CCGGGANGGG	480
CATCAGGAAG	TGAGTCTTCA	TCTCCAGGG	CGTGNAGGTG	GGTNCCATGA	CCAGCTTCCT	540
AATGACCTGG	GAGCCATGGG	GAACGTGGGC	ATCTCCACCA	GAGCTACTGG	GCACAGGTTT	600
CTCGACCGTG	TGTGGNCGCA	CAGACCGTCG	ACGGCCTCTT	TGNCCCTCGA	GACA	654

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GTCGACCTGA	GAATCTGGAA	AAATTGGAGA	AGTTGGGTAT	GAGCTCAGAC	CTGGTGAGCA	60
GGTGCCTTAC	CATTTATAGA	AATGCACATG	ACATCAAGAA	TAAGAGCTCT	GCCCCCAGCA	120
GAGTGCCTCC	TCTTTTGTG	CCACAGGGGA	CTTCTGAAAG	AAAAGACAGT	TCAGGTTCTG	180
TGTCCCCAMA	CACCTCTAGC	CAGGAGGAGG	GTGATCAGAT	CTGTTTGTKC	CATATCCGGA	240
AAAGTTGTAG	CTTTCAAGAT	AAGTGCCATA	GAGTTCATTT	CCATTGSCCG	YATCGATGGC	300
AATTCTTGGA	TAGAGGCAAA	TGGGAGGATT	TGGACNACAT	GGAACNTATT	GTAGAGNCAT	360
ATTGCAATCC	CCCCATAGAA	AGGATCCTGT	GCTCTGAGTC	AGCCAGTACC	TTTCACTCTC	420
ATTGTCTGAA	CTNTAACGCC	ATGACTTACG	GTGCTACCCA	GGCTCGCCGC	CTCTCCACGG	480
CCTCTTTGGC	CCTCGAGACA					500

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTCGACACAA	ATGTTTCCTT	GGATAATCCA	GCTTTACATG	GTGAGAACCA	TGCTAGAGTC	60
CCTCATTGCA	GACAAAAGTG	GTTCCAAGAA	AACCTTGAGA	AGTAGCCTTG	AGGGGCCCCAC	120
CATATTGGAC	ATAGAAAAAT	TTCATCGAGA	GTCATTCTTC	TACACTCACT	TGATAAATTT	180
CAGTGAAACG	CTGCAGCAGT	GCTGTGACCT	TTCGCAGCTG	TGTTTCCGAG	AGTTCTTCCT	240
GGAGCTGACC	ATGGGCAGGA	GGATCCAGTT	CCCCATTGAG	ATGTCGATGC	CCTGGATCCT	300
GACGGACCAC	ATCCTGGAGA	CCAAGGAGGC	ATCGATGATG	GAGTACGTGC	TCTACTCCCT	360
GGACCTGTAC	AATGACAGCG	CCCCTACGCG	GCTCACCAGG	TTCAACAAGC	AGTTCTCTTA	420
CGACGAAATT	GAGGCCGAGG	TCACGGCCTC	TTGGCCCTC	GAGACA		466

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

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GTCGACGGAA GTTGATTTTT AATGATAAAG TACAATGAAG GGAGGGCAGA GGGGCTAAGC    60
CTAGCTGTCT GGGGTGCTGT GGTGGTGGTA GACTGGCTAC ACAAAGTGTG GCTGCTGCTG    120
CTGCTTCTTG GTGGCCGCCT TGCTGGCGAG GTCTTGCC TTCTCTGTAG CTGCCAGTGC    180
CGTCTCCTTT GCCTTCTCCT TGGCTTCCTT GGCTGTCTCA ACAAGTGTG TGAAGGGGC    240
CTCGCCTTGC AGCTTAGCCA AGATATATTC AAAACCCCTC ATAGTCTTGG TCACGTTGCT    300
TTTGAACCGG GCAAGACCAA ATCCTGGAC AGCTCTGGCT ACACAACTG TTGCTGGTCA    360
ACGGCCTCTT TGGCCCTCGA GACA

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(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

GTGACGGGAC AAAAATCTAG GGAGGCACCA ATCCTGAAAG AGTTTAAGGA AGAAGGGGAA    60
GAGATACCTA GAGTAAAACC AGAGGAGATG ATGGATGAGA GACCCAAAAC AAGATCCCAG    120
GAACAGGAGG TGTTAGAGAG AGGAGGGAGA TTTACAAGAT CCCAGGAAGA GGCTAGAAAA    180
AGTCATCTGG CCAGACAGCA GCAGGAGAAG GAAATGAAAA CAACATCTCC CCTTGAGGAG    240
GAAGAAAGAG AAATAAAATC TTCACAAGGC TTAAAGGAAA AATCGAAGTC TCCTTCCCCT    300
CCTCGACTGA CTGAAGATCG AAAGAAGGCC CCACTTGTAG CGCTGCCAGA GCAAAGTGGC    360
AGCGAGGAGG AGACTCCTCC ACCTTTACTA ACAAAGGAAG CATCTTCTCC ACCACCTCAT    420
CCACAGCTCC ATAGCGAAGA AGAAATAGAG CCCATGGAAG GCCCAGCCCC CCCTGTCTC    480
ATTCAGTTAT CTCCTCCTAA TACAGATGCT GACACCAGGT CGACGGCCTC TTTGGCCCTC    540
GAGACA

```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

GTCGACGTCG GTGGTGCGAG CGGCGGCGGC GCGGTTCCA GCATGAAGAG GAGAGCTGGC    60
CTGGGGGGCA GCATGAGGTC AGTGGTGGGC TTCTGTCCC AGCGGGGCTC GCATGGGGAC    120
CCCTGTCTCA CTCAGACTT TCAGAGGAGA CRCCTGCGGG GCTGCAGAAA CCTCTACAAG    180
AAGGACCTCC TCGGCCACTT CGGCTGTGTC AATGCCATTG AATTCTCAA CAATGGAGGC    240
CAGTGGCTGG TCTCAGGAGG AGATGACCGC CGGTTCTGCT TATGGCACAT GGAACAAGCC    300
ATCCACTCCA GGGTCAAGCC CATACAGCTG AAAGGAGAGC ACCATTCAA CATTTTTTGC    360

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CTGGCTTTCA ACAGTGGGTA CACTAAAGTG TTCTCTGGAG GCAATGATGA GCAAGTTATC	420
CTCCATGATG TTGNAAGCAG TGAGACATTG GACGTGTTTG CTCATGAAGA TGCAGTATAT	480
GACTTGCTCTG TGGTCNGCGC CCTCTTTGGC CCTCGAGACA	520

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTGCGACTCCA GACACACCCC CCAGTCGAGC CCTGCAGCCA AACAGAGCCT TCACAACCAG	60
CCACACAGAG CCTGCCTCAG CTGCTCGCAC AGATTACTTC AGGGCTGGAA AAGTCACACA	120
GACACACAAA ATGTCACAAAT CCTGTCCCTC ACTCAACACA AACCCCAAAG CACAGAGAGC	180
CTGCCTCAGT ACACTCAAAC AACCTCAAAG CTGCATCATC ACACAATCAC ACACAAGCAC	240
AGCCCTGACA ACCCACACAC CCCAAGGCAC GCACCCACAG CCAGCCTCAG GGCCACAGG	300
GGCACTGTCA ACACAGGGGT GTGCCAGAG GCCTACACAG AAGCAGCGTC AGTACCCTCA	360
GGATCTGAGG TCCCAACACG TGCTCGCTCA CACACACGGC CTGTTAGAAT TCACCTGTGT	420
ATCTCACGCA TATGCACACG CACAGCCCTC AACGGCCTCT TTGGCCCTCG AGACA	475

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCTGCCACAA TAATNTCCNA AGCCTAAAC CCGAGCAATA CAANCNAACC CAAGCTCGGA	60
AATCGGGCCA AAGAGACCGT TCTTAGNTGG TGGAGCGATT TGTCTGGTTN ATTCCGATAA	120
ACGAACGAGA CTCTGGCATG CTAAGTAGTT ACGCGACCCC CGAGCGGTCG GCGTCCCCCA	180
ACTTCTTAGA GGGACAAGTG NCGTTCANCC CACCCGAGAT TGAGCAATAA CAGGTCTGTG	240
ATGCCCTTAG ATGTCCGGGG CTGCACGCGC GCTACACTGA CTGGCTCAGC GTGTGCCTAC	300
CCTACGCCGG CAGGCGCGGG TAACCCGTTG AACCCCATTC GTGATGGGGA TCGGGGATTG	360
CAATTATTCC CCATGAACGA GGAATTCCCA GTAAGTGCGG GTCATAAGCT TCGGTTGATT	420
AAGTCCCTGT CGACGGCCTC TTTGGCCCTC GAGACA	456

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GTGCGRRCAA SMTYTYTMMA CTGTGGNGGG GCTCTACCCN TGAGGGCCTG GCCGCARCNT	60
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GGCTGSGGGC	TGWCGACTAT	GAACAGRTCG	AGAAMGTGKN	CGATTACTAC	CCGGAGTACA	120
AGCTRCTCTY	CGAGGGTGCA	GGTAGGCAAC	CCTGGAGACA	TGACKCTGGA	GGGMCGATTA	180
CTTTGAGYAC	GAGGTAAARC	TGAACAAGTT	GTSCCTTCCTG	ANACAGTWCC	ACCTTGGTGT	240
CTTCTATRCC	TTCGTGAAGC	TCAAGGAGCA	GGAGTGTCKC	AACATCGTGT	GGATCGCTGA	300
ATGTATCTRC	CAACGCMSS	GCRMMYCSMA	MSWCAWCCWY	ATTCTSTRTC	CTKSYAASGT	360
CWCAMTGAAN	CWAGCCCTCT	CAATTGCACT	GCACTGTGTG	TGTGTGTGTG	TGTGTTGTGC	420
GTGTGTGTTG	CGTGTGTGTG	TATGTGGTCT	GTGACAAGCC	TGTGGCTCAC	CTGGTCGACG	480
GCCTCTTTGG	CCCTCGAGAC	A				501

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCNCCGTTTG	TTGTNNTGCA	CCAAANANCC	NCNAATTGNC	CANANAAAAT	TGATGGGAAG	60
ACCACTTAAA	GGGGGGGNAN	TTAGGCGGGN	CAAAGACAAG	GCACCCNACA	AGATGTCGTT	120
TGTTCCAGAG	CTGATTGAGG	GGTATCTCGG	AAGNAACACN	GAAACTTTTT	TCCTTCCTTC	180
AATTCAACGC	ACACTACTCT	CTAATGAGCN	NCGGAATACG	GCCTTCCTTC	CAGTTACTTG	240
AATNTGAAAT	AAAAAAAAGT	TTGCTGTCTT	GCTATCCAAG	TATAAATAGA	CCTGCAATTA	300
TTAATCTTTT	GTTTCCTCGT	CATTGTTCTC	GTTCCCTTTC	TTCCTTGTTT	CTTTTCTGTC	360
ACAATATTTT	AAGCTATACC	AAGCATACAA	TCAACTCCAA	GCTCGGAATT	CGGCCAAAGA	420
GGCCGTCGAC	GAACCACCGG	CTGAAAATTG	GCTTCTTCAA	CCAGCAGTAT	GCAGAGCAGC	480
TGCGCATGGA	GGAGACGCCC	ACTGAGTACC	TGCAGCGGGG	CTTCAACCTG	CCCTACCAGG	540
ATGCCCCGCA	GTGCTTGGGC	CGCTTTGGCC	CTCGAGACA			579

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCTGCNCCAA	NANTTCCNAA	CCNAATAACC	CAANAANACC	AATCCNNNCT	CCANCTGGGG	60
AATTCGGNCC	NAAGAGACCG	TTGTNTTGAT	GACAAGTCGA	AGCCAANAAT	ACCATNCAAC	120
CTGCTCCCAA	TCATGCAGGN	TNCNGCCACT	GCTGCCCTTG	CCGTCCCTCC	TCTGCACCAT	180
GGCTNCTCCT	GCAACCAGGT	CCTCTCTGCA	CCAATTGCTG	CTGANACGCC	GACCGCTGTC	240
TGCTTCAGCT	ACACCTCCCG	ACAGATTCCA	CAGAATTTC	TAGCTGACTA	CTTTGAGACG	300
AGCAGCCAGT	ACTCCAAGCC	CAGTGTATC	TTCCTAACCA	AGAGAGGCCG	GCAGGTCTGT	360
NNTGACCCCA	GTGAGGAGTG	GGTCCAGAAA	TACGTCAGTG	ACCTGGAGCT	GAGTGCCAGA	420
GGGGTCCAGA	AGCTTCGAGG	CCCAGCGACC	TCAGTGGGCC	CAGTGGGGAG	GAGCAGGAGC	480
CTGANCTTGG	GGAACATGCG	TGTGACCTCT	ACAGCTACCT	CGTCGACGGC	CTCTTTGGCC	540
CTCGAGACA						549

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GTCGACCTCC	CAGGTCATTA	GGAAGCTGGT	CATGGAACCC	ACCTTCAAGC	CCTGGCAGAT	60
GAAGACTCAC	TTCTGATGC	CCTTCCCGGT	GAATTACGTG	GGTGAATGCA	TCCGAACTGT	120
CCCCTACACG	GACCCAGATC	ATGCCAGTCT	TAAATCCTT	GCACGTTTGA	TGACTGCCAA	180
ATTCTTGCAT	ACAGAAATT	GTGAAAAAGG	CGGTGCTTAT	GGTGGAGGCG	CAAAACTCAG	240
CCACAATGGG	ATTTTACCC	TTTACTCTTA	CAGGGACCCA	AATACAATAG	AGACGCTCCA	300
GTCTTTTGGG	AAGGCTGTCG	ACTGGGCTAA	GTCTGGAAAA	TTACACAGC	AAGACATCGA	360
CGAAGCCAAA	CTTTCTGTCT	TCTCAACCGT	AGATGCTCCT	GTCGCTCCTT	CAGACAAAGG	420
AATGGACCAC	TTCTGTACG	GCCTCTTTGG	CCCTCGAGAC	A		461

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 511 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GTCGACAATA	ATTCCACCTC	ACCAGGATAA	TACCCATCCT	TCAGCACCAA	TGCCTCCACC	60
TTCTGTTGTG	ATACTGAATT	CAACTCTAAT	ACACAGCAAC	AGAAAATCAA	AACCTGAGTG	120
GTCACGTGAT	AGTCATAACC	CTAGCACTGT	ACTGGCAAGC	CAGGCCAGTG	GTCAGCCAAA	180
CAAGATGCAG	ACTTTGACAC	AGGACCAGTC	TCAAGCCAAA	CTGGAAGACT	TCTTTGTCTA	240
CCCAGCTGAA	CAGCCCCAGA	TTGAGAAAGT	TGAAGAGTCA	AACCCATCTG	CAAAGGAAGA	300
CAGTAACCC	AATTCTAGTG	GAGAAGATGC	TTTCAAAGAA	ATCTTTCAAT	CCAATTCACC	360
GGAAGAATCT	GAATTCGCCG	TGCAAGCGCC	TGGGTCTCCC	CTAGTGGCTT	CCTCTTTATT	420
AGCTCCTAGC	AGTGGCCTTT	CAGTTCAAAC	TTCCCACCAG	GGCTTTACTG	CAAAACAAGC	480
ACGGTCAACG	GCCTCTTTGG	CCCTCGAGAC	A			511

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTCGACAGTC	CAAAGTCTCA	AGACAGTTAT	CCTGTTAGTC	CTCGACCTTT	TAGTAGTCCA	60
AGTATGAGCC	CCAGCCATGG	AATGAATATC	CACAATTTAG	CATCAGGCAA	AGGAAGCACC	120
GCACATTTT	CAGGTTTGA	AAGTTGTAGT	AATGGTGTAA	TATCAAATAA	AGCACATCAA	180
TCATATTGCC	ATAGTAATAA	ACACCAGTCA	TCCAACCTGA	ATGTACCAGA	ACTAAACAGT	240
ATAAATATGT	CAAGATCACA	GCAAGTTAAT	AACCTCACCA	GTAATGATGT	AGACATGGAA	300
ACAGATCACT	ACTCCAATGG	AGTTGSAGAA	ACTTCATCCA	ATGGTTTCCT	AAATGGTAGC	360
TCTAAACATG	ACCACGAAAT	GGAAGATTGT	GACACCGAAA	TGGAAGTTGA	TTCAAGTCAG	420
TTGAGACGCC	AGTTGTGTGG	AGGAAGTCAG	GCCGCGTCTA	CGGCCTCTTT	GGCCCTCGAG	480
ACA						483

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

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GTCGACGAGG TGGTGATCAT GGAAGACGCC CCTGACTATT ATGCAGTGGA AGACATTTTC      60
AGCGAGATCT CAGACATTGA TGAGACAATT CATGACATCA AGATCTCTGA CTTCATGGAG      120
ACCACCGACT ACTTCGAGAC CACTGACAAT GAGATAACTG ACATCAATGA GAACATCTGC      180
GACAGCGAGA ATCCTGACCA CAATGAGGTC CCCAACAACG AGACCACTGA TAACAACGAG      240
AGTGCTGATG ACCACGAAAC CACTGACAAC AATGAGAGTG CAGATGACAA CAACGAGAAT      300
CCTGAAGACA ATAACAAGAA CACTGATGAC AACGAAGAGA ACCCTAACAA CAACGAGAAC      360
ACTTACGGCA ACAACTTCTT CAAAGGTGGC TTCTGGGGCA GCCATGGCAA CAACCAGGAC      420
AGCAGCGACA GTGACAATGA AGCAGATGAG GCCAGTGATG ATGAAGATAA TGATGGCAAC      480
GAAGGTGACA ATGAGGTCAC GGCCTCTTTG GCCCTCGAGA CA                          522

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(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

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GTCGACAGAT CATGTTGGAA GAGCCCCCAG TAGCAAAAGT GTTAGAGCCT TCAGAAACCC      60
TTGTGGTATC ATCAGAGACA CCTACTGAGG TGTACCCTGA GCCAAGCACA TCAACAACAA      120
TGGATTTTCC AGAGTCATCT GCAATTGAAG CGCTAAGATT GCCAGAGCAG CCTGTAGACG      180
TACCATCGGA GATTGCAGAT TCATCCATGA CAAGACCGCA GGAGTTGCCG GAGCTGCCTA      240
AGACCCACAGC GTTGGAGCTG CAGGAGTCGT CGGTGGCCTC AGCGATGGAG TTGCCGGGGC      300
CACCTGCGAC CTCCATGCCG GAGTTGCAGG GGCCCCCTGT GACTCCAGTG CTGGAGTTAC      360
CTGGGCCCTC TGCTACCCCG GTGCCAGAGT TGCCAGGGCC CCTTCTACC CCAGTGCCTG      420
AGTTGCCAGG GCCCCCTGCG ACAGCAGTGC CTGAGTTGCC AGGGCCCTCT GTGACACCAG      480
TGCCACAGTT GTCGAGGAA TTGCCGTCAA CGGCCTCTTT GGCCCTCGAG ACA                          533

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(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

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CCACCAGACA TAAAGTACTG ACATGATCAG AGGAATCATC AGCAACTGCA TNTCCATTGC      60
TAAGCCAGTA ATCACGATGC AAATCCAGTT AAAGAGGAGC ATGAATAAAT AGTCTGCTGG      120
CCTCCCATCA AAAGCTCCTG TTCAAGTCG CGTAGAATAC TGATATAAGA AATATANATT      180

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GACCAAATAA	AGAAATCCAG	TTCCTGGACC	CACAGGGAAA	TAAAAGGTGG	CAGTGATTGN	240
CCTCCAAATC	TGAAAGCGAT	ANAGGAAGGC	TTCGGGCCAG	AGGAAGAGGT	AGGCCGGGCT	300
GATGAGGCCG	AGTTTGCCGA	CCAAGGGCAC	GGNGACGGTG	GCGGCGAACC	AATAGCGCGT	360
GATCGCCGGG	ATGCTCCTGA	ACCAGTCTCC	GATGTCCGAC	ATCTTCGACC	CACAGGTAGC	420
CAAGATGCAC	AAGACCGCCC	GACTCCCCGC	GCCGACCCCC	TCACGACGCG	GCCGGCTCCG	480
CGACTGTTAG	GTGTCTAGGT	GGAAGCCGCG	TCGAC			515

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATNCNGGAGN	CCCAGATGCT	GTGGGCCCATG	ATCGCANNTT	GNNTGAGAGA	ATTGGCAGAA	60
NCAGANTACT	CCTAGCNAGA	NCAGTATTNT	GTGTNACTCT	GGAGAATTNC	AGTGATGNAA	120
AAAAANAGAC	CNGTNCAAGT	AAGTCCAGCG	AAAAGCATGC	CCACATGGAT	GAANTGGATG	180
ATGAAGATGA	TGCCNNCCNT	GNGGNCAGCA	GGAACCTCTN	TNNCTGCGNG	NCNACTCNTG	240
NTGNTGTAGA	TGANGCTGGT	NAAGCNNANC	AGTCTGNTGA	GNCTCCTCGA	GTCTGATGGA	300
TCTNATGAGC	AGANCGNTGA	TTCGTGNGCC	GCCGTNCTCC	TTNGAGCCCN	CNAGACA	357

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTTGATAGATG	GAGCGGGGAG	NCAGACTNCT	GGGNGCTGCG	TGANTGCTGA	CGTGAGATGG	60
ATTAATTAAT	GGCNAGCAAG	NATGGNGNCT	NCGAGCCCCCT	CCCTGNNCGT	NCCTNCCAGN	120
NGTGGCAATN	GCGTACGTGG	NCAGACTTCA	GGNAGAAAAA	AAAAAAANGG	GNCNCGTAAG	180
CTGCTGCGGG	NNCAGCAGCT	TGAGACTGNC	AAGTGACTCA	GATGCAGAGT	CAGACTNTCG	240
GGCTAGCTCT	AACAACTCCN	CCGTCTCCAA	CACCAGCACC	GAGGGCTTCG	GGGACATCAT	300
GTCTTTGACC	AGCAGCCTCT	ATCGGAACCA	CAGTACCAGC	TTCACTCTTT	CAACCTCAC	360
ACTNCCGTCG	NCGGCCTCNT	TGGCCTTTNG	AGGC GA			396

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GTCGACCCCA	GATGAAATGT	CATGGCAAAT	TTGATAAAAA	CCAAGAGGGA	GTGAAACTGA	60
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CGCTGGGGGA	GGGAAGGGTC	AAGTCGAGGG	AAGGTGAAAC	CAAAAGGCAC	TGAGCATGCG	120
TGGTGGGGCA	GGGAAGGACA	CCATCACTCC	AGAGACAGTA	TGGTAACAAA	GGGACAGGAA	180
TGGTCCAGGC	CAGCTTCAGG	CTCTTCAGAA	GCCAGAGAGA	TGTCCAAGTC	TACCAAACCG	240
AGTTCTCCAA	GGCTTTTCAA	GAAATGGGAT	TTGCTTGCAA	GATGAATGAG	GGAGGAGGTC	300
CCATGGCTTC	TAAGAGATCA	ACCCAAGTCT	TCCAATACTC	ACTGCTAAGT	CCCACCTGGG	360
TCCCCCAGAG	CCAGGAAGCT	CCCTGGTGGC	AGGTCCCCCT	CTTGCCCTCA	CGGCCTCTTT	420
GGCCCTCGAG	ACA					433

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTCCACAAAA	TAGTTCTGTT	AAAGAATACC	GAATGGAAGT	TCCATCTTCG	TTTTCAGAAG	60
ACATGTCAAA	TATCAGGTCA	CAGCATGCAG	AAGAACAGTC	CAACAATGGT	AGATATGACG	120
ATTGTAAAGA	ATTTAAAGAC	CTCCACTGTT	CCAAGGATTC	TACCCTAGCT	GAGGAAGAAT	180
CTGGGTTCCC	TTCTACTTCT	ATCTCTGCAG	TTCTGTCTGA	CTTAGCTGAC	TTGAGAAGCT	240
GTGATGGCCA	AGCTTTGCC	TCCCAGGACC	CTGAGGTTGC	TTTATCTCTC	AGTTGTGGCC	300
GTTCCAGAGG	ACTCTTTAGT	CATATGCAGC	AACATGACAT	TTTAGATAACC	CTGTGTAGGA	360
CCATTGAATC	TACAATCCAT	GTCTGCACAA	GGATATCTGG	CAAAGGAAAC	CAAGCTGCTT	420
CTTGGTCAAC	GGCCTCTTTG	GCCCTCGAGA	CA			452

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTNAAANTTA	CCATCACAGT	TNCTACAATC	GGCTCTTCC	AATTTGGCNA	CAACNCTGGG	60
TCATCAATGC	TCCTGAGAAG	ATCATAAAGG	AATTTATCAA	TAAAACTTTG	TCGGACAAGG	120
GAAATNCCCC	ACCCTCTGAG	GTGCTGCTCA	CGTCTCTCTG	GTCCTTGCTT	GTGACCATAT	180
TTTCCGTCGG	GGGNATGATC	GGCTCCTTTT	CCGTCGGACT	CTTCGTCAAC	CGCTTTGGCA	240
GGCGCAANNC	AATGCTGATT	GTCAACCTGT	TGGCTGTCAC	TGGTGGCTGC	TTTATGGGAC	300
TGTGTAAAGT	AGCTAAGTCG	GTTGAAATGC	TGATCCTGGG	TCGCTTGGTT	ATTGGCCTCT	360
TCTGCCGACT	CTGGTCGACG	GCCTCTTTGG	CCCTCGAGAC	A		401

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTTGAGAGCA	GCATGTTTTN	NCCACTGAAA	CTCATCCTGC	TGCCAGTGTT	ACTGGATTAT	60
TCCTTGGGCC	TGAATGACTT	GAATGTTTCC	CCGCCTGAGC	TAACAGTCCA	TGTGGGTGAT	120
TCAACTCTGA	TGGGATGTGT	TTCCAGAGC	ACAGAAGACA	AATGTATATT	CAAGATAGAC	180
TGGACTCTGT	CACCAGGAGA	GCACGCCAAG	GACGAATATG	TGCTATACTA	TTACTCCAAT	240
CTCAGTGTGC	CTATTGGGCG	CTTCCAGAAC	CGCGTACACT	TGATGGGGGA	CATCTTATGC	300
AATGATGGCT	CTCTCCTGCT	CCAAGATGTG	CAAGAGGCTG	ACCAGGGAAC	CTATATCTGT	360
GAAATCCGCC	TCAAAGGGGA	GAGCCAGGTG	TTCAAGAAGG	CGGTGGTACC	GCATGTGCTT	420
CCAGAGGAGC	CCAAAGAGCT	CATGGTCCAT	GTGGGTGGAT	TGATTCAGAT	GGGATGTGTT	480
TTCCAGAGCA	CAGAAGTGAA	ACACGTGACC	AAGSTAGAAT	GGATATTTTC	GTCGACGGCC	540
TCTTTGGCCC	TCGAGACA					558

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GTGGAGAAAA	TTGCTGCTGA	GAAGGACATT	TTGAAGGTTT	TGTTGGCTGA	AAAAGCTGTT	60
TCTGGAATCA	CCCCTAGATC	TTTCTTGAAG	ACTTGAATTA	GATTACAGCG	ATGGGGACAC	120
AGAAGGTCAC	CCCAGCTCTG	ATATTTGCCA	TCACAGTTGC	TACAATCGGC	TCTTTCCAAT	180
TTGGCTACAA	CACTGGGGTC	ATCAATGCTC	CTGAGAAGAT	CATAAAGGAA	TTTATCAATA	240
AAACTTTGAC	GGACAAGGGA	AATGCCCCAC	CCTCTGAGGT	GCTGCTCAG	TCTCTCTGGT	300
CCTTGTCTGT	GGCCATATTT	TCCGTGCGGG	GTATGATCGG	CTCCTTTTCC	GTCGGACTCT	360
TCGTCAACCG	CTTTGGCAGG	CGCAANTCAA	TGCTGATTGT	CAACCTGTTG	GCTGTCACTG	420
TGACTGCTT	TATGGGACTG	TGTAAAGTAG	CTAAGTCGGT	TGAAATGCTG	ATCCTGGGTC	480
GCTTGGTTAT	TGGCCTCTTC	TGCGGACTCT	GGTCGACGGC	CTCTTTGGCC	CTCGAGACA	539

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GTTGACCCCA	TTTTCCACCA	CCAAGCAAGC	AGAGCCTGTT	GTTTTGTCCA	AAATCAAAAC	60
TGCACATCCA	CAGAGCAGAG	ATCTCAAAGA	TTATGCGAGA	ATGTCAGGAA	GAAAGTTTCT	120
GGAAGAGAGC	TCTGCCTTTT	TCTCTTGTA	GCATGCTTGT	CACCCAGGGA	CTAGTCTACC	180
AAGGTTATTT	GGCAGCTAAT	TCTAGATTG	GACCATTGCC	CAAAGTTGCA	CTTGCTGGTC	240
TCTTGGGATT	TGGCCTTGGA	AAGGTATCAT	ACATAGGAGT	ATGCCAGAGT	AAATTCCATT	300
TTTTTGAAGA	TCAGCTCCGT	GGGGCTGGTT	TTGGTCCGTC	GACGGCCTCT	TTGGCCCTCG	360
AGACA						365

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GTCGACCTCG	GTAAATGCCT	CAGTTCCCCT	CCCAGATGGA	GGCATCGTTG	TGAGAGTCTG	60
ATTGGGAGGG	GAATATGAAA	ATGTTTTCGG	AAGATAAAAG	TACTACACAG	ATGTGAGGTG	120
GTTTTGCCTT	GGAAGAAAGT	GTCCTTAGA	TGTGCTGGA	TGTTATGCAG	AGTGATCGTG	180
GCGTGTCAAT	CTTTCTTTTG	GGTGTTTTGC	AGCCTGAGAC	ATAAGGTAAT	TGTCAGAAAA	240
GGGAGACGTA	GAAGTGTGGA	TCTGTGGAAG	CTCACTCTTA	ACAAGAATTC	TAAGATGCAC	300
ATTTAAGTAC	TTGCCATGAC	GTGAGGTGTT	GTCACACGTC	AACCCTGAGA	TGCTGTCAGT	360
GTCCCAGGGG	ACTTGACATT	TATGTTACCC	AGGAATGACT	GTGTAAATGT	GCAGGTGCAG	420
GCCGGGCGCC	GTGGCTCAGT	GCCTGTAATC	CCAGCACTTT	GGGAGCCCCG	TCGACGGCCT	480
CTTTGGCCCT	CGAGACA					497

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GTAGACANCA	NTAGAAAAAC	AAAAATCTCA	TAATGCAAAA	GCATCAAGTG	TTTACTCTG	60
AGAAGCGCCT	TGTATGCCCC	GTTACTCTCG	TTCTCCCTCA	GCTCTTGCTT	GTGCTTCTCC	120
ACCTGCCATT	CCACTTTGGC	CTGGTACTGC	CTGTAGTCTT	CCTGGCAGGC	CCCAGCTCCA	180
GTTCTTTGGA	GCAGCTGGGC	ATCCAAGAAG	AGGTCATTGC	TGTGGAAGGA	GCCCTCTCGC	240
TCCCTCCCCA	GCCTCTCAAT	CACAGCCAGG	AGCTCTGCCT	GCTGCTGCCT	CTGCTCCTCC	300
ACAGAGCCCC	AGTTGTTGAA	GGCACAGTAC	CTTCTCTCAC	ACTCCCGCGC	CAGGTCTTTC	360
AGGCTGCAGT	TGTCCGTGTT	TGCTACATAG	TCATCCAGGG	CCTGGCCCCG	TCGACGGCCT	420
CTTTGGCCCT	CGAGACA					437

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CCTGCNCNAA	ANNANTCCAA	GCNAANNCCC	AAACAATCCC	AATNCCNACC	CCAAGCTNNG	60
GAGTTCGGCC	CAAAAGAGGC	CCNNCGAACG	TAGATTNCAG	TGAGCCAAGA	TCGTNCCACT	120
GCACNCCAAG	CCNGGGCANC	CAAGAGCGAA	ACTCCGTCNC	CNCNNNANAA	AGAGAAAATT	180
AGCCGGGCGT	GGTGGCGTTA	ATCCCANCTA	CTTGTGAGGN	TAAGGGAGGA	.GAATTGCTTG	240
AACCCAGGAG	GCAGAGGTTG	CAGTGAGCTG	AGATCACGCC	ATTGCACTCC	AGCCTGGGCC	300
ACAAGAGCAA	GACTCCATCT	CCCCAAAAAA	AAAAAAATAG	CGTCAGAAAA	ATGTCCTTGT	360
ATGCCATTTT	CTCCATTTTA	TTGACATTTT	GCCCCACTTT	TGTCCTTGTT	TCAGGGAAAT	420
CGTGGAACAC	ATGGTCCAGC	ACTTTAAAAC	ACAGATCTTT	GGGGATCGGA	AGCCCGTGTT	480
TGACGGCAGG	GTCAACGGCC	TCTTTGNCCC	TCGAGACA			518

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

AAACCAAAC TCATGTTGCT TGNCCCCCA TCGTCGTCTC AAGTGNGGGC GANNACTTTC      60
CTGGTTGGAG CCTCCGTCC NAACNNCTAA CACAATGTTT TTTCNCAAAC GTTCTACNAA      120
CGCCTGCGAC NAGNCCAGGG AGGGGGTGCT GTGNATCCTC AGCNACGACA CGCTGCAGTA      180
CTGCGACTTC TTGGGCTCCG GGGCGGCCAT CTGGGTCACC ATNCTGTGNA TGGCACGGCT      240
CAAGACAGTC CTGAAATACG TGCTGTTTCT TCTGGGTACA CTGGTCATCT CCATGTCCTT      300
GCAGCTGGAC CGCAGGGGCA TGTGGAACAT NCTGGGGCCC TCCCTCTTTG CCTTCGTGAT      360
CATGGCCTCC ATGTGGGCTT ACCGCTGCGG GCACCGGCGC CAGTGCTACC CCACCTCGTG      420
GCAGCGCTGG GCCTTCTACC TCCTGCCCGG CGTCTCTACG GCCTCTTTGN CCCTCGAGAC      480
A

```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

GACCCTCCAN TAATAANCCT TTTGTTTCCC TCGTCNNTGT TNGTCCGTTC CCCTTTCCTN      60
CCCTTGTTTC NNTNTCTGTC ACCAATATTT CCAANCTAAT ACCCAAGCAA NACAATCCNA      120
ACTCCAAGCT CGGGAATTCG GCCCAAAGAG ACCGTAGGCC GAAACCCACC GGANGGAACC      180
ATCTCACTGT GTGTAAACAT GACTNCCAAG CTGNCCGTGG CTCTCTTGGC AGCCTTCCTG      240
ATTTCTGCAG CTCTGTGTGA AGGTGCAGTT TTNCCAAGGA GTGCTAAAGA ACTTAGATGT      300
CAGTGCATAA AGACATACTC CAAACCTTTC CACCCCAAAT TTATCAAAGA ACTGAGAGTG      360
ATTGAGAGTG GACCACACTG CGCCAACACA GAAATTATTG TAAAGCTTTC TGATGGAAGA      420
GAGCTCTGTC TGGACCCCAA GGAAACTGG GTGCAGAGGG TTGTGGAGAA GTTNTGGAAG      480
AGGGCGTCGA CGGCCTCTTT GGCCCTCGAG ACA

```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

CAANTAATAA ANCTTTTGTT TCCCTCGNCA TTGTNNTCGT TCCCCTGTCC NGCCTTGTTT      60
CCNNNGTCCT GCACCAATAT TTCCAAACCN AATACCCAAG CATACAATCC NNACTCCAAG      120
CTNGGAATTC GCCCANAGAG ACCGTCGNGG GAAGAANTTG NCTGGAAACT TGTCATGGT      180

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GATATATACC	GTCCTCCAAG	AAANGGGATG	CTGCTATCAG	TCTTTCTAGG	AGCCGGGANA	240
CAGATATTAA	TTATGACCTT	TGTGACTCTA	TTTTTCGCTT	GCCTGGGAGT	TTGTGCACCT	300
CCCANCCGAG	GAGCGCTGAT	GACGTGTGCT	GTGGTCCTGT	GGGTGCTGCT	GGGCACCCCT	360
GCAGGCTATG	TNCTGCCAG	ATTCTATAAG	TCCTTTGGAG	GTGAGAAGTG	GAAAACAAAT	420
GTTTTATTAA	CATCATTTCT	TTGTCCTGGG	ATTGTATTTG	CTGACTTCTT	TATAATGAAT	480
CTGATCCTCT	GGTCAACGGC	CTCTTTGGCC	CTCGAGACA			519

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CGGGCCCAAA	GACANGCANN	CCNACAAGAT	GTCGTGTTC	CAAGAAGCTG	ATNGAGGGGT	60
ATCTCGGAAG	CACACGGAAA	CTTTTCCTT	CCTTCAATTC	NACGCACACT	AACCTCTTAA	120
TGAGCAANCG	GTATACGGCC	TTCTTCCAG	TTACTGNAT	GTGAAATAAA	AAAAAGTTG	180
CTGTCTTGCT	ATCAAGTATA	AATAGACCTN	CAATTATTAA	TCTTTTGTTT	CCTCGTCATT	240
GTTCTCGTTC	CCTTCTTCC	TTGTTTCTT	TTCTGCACAA	TATNTCAAGC	TATACCAAGC	300
ATACAATCAA	CTCCAAGCTC	GGAATTCGGC	CNAAGAGGCC	GTCGACCGTT	CGTTATCGGA	360
ATTAACCAAG	CAAATCGCTC	CACCAACTAA	GAGCGNCCAT	GCACCACCAC	CCACGGAATC	420
GAGAAAGAGC	TATCAATCTG	TTGAAGAACA	TGCCCGGCTT	CTTGGTCATC	ATCATGGTGT	480
ACACGNCCTC	TTTGNCCCTC	GAGACA				506

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TTCTTGTTT	CCTTTTCCT	NCCCCAATAT	TTCCAAGCTA	ATACCCAAGC	AATACAATCC	60
NACTCCAANC	TCGGGAATTC	GGCCCCAGAG	GACCGNTGAC	CNTGTAAATG	AGTGAGGCAG	120
GAGTCCCGNG	GAGGTAGTT	GTGTCAATAA	AAATGATTAA	GGATACTAGT	ATAAGAGATC	180
AGGNTCGTCC	TNTAGTGTG	TGTATGGNTA	TCATTTGTTT	TGAGGNTAGT	TTGATTAGTC	240
ATTGTTGGGT	GGTGATTAGT	CGGTGTGTTA	TGAGATATNT	GGAGGTGGGG	ATCAATAGAG	300
GGGGANATAG	AATGATCAGT	ACTCCGNCAG	GTAGGCCTAG	GATTGTGGGG	GCAATGAATG	360
AAGCGAACAG	ATTTTCGTTT	ATTTTGGTTC	TCAGGGTTTG	TTATAATTTT	TTATTTTTAT	420
GGNCTTTGGT	GAGGGAGGTA	GGTGGTAGTT	TGTGTTTAAT	ACAAAAAGTT	GGGTCGACGN	480
CCTCTTTGNC	CCTCGAGACA					500

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

AACCGGATTC GGNCCNAAAG AGACCGGTTG CCCAAACTT TCTGCTGAGA AGGACATTTT      60
GGAGGGGNTT TGTGGGGCTG AAAAAAGCT GTTCCTGGG AATNNAACCC CCNAGANCTT      120
TCTGAAGAC NTTGAATTAA GATTACCAAN CGATGGGGGA CACAGGAAGG TCCACCCCA      180
NGCTCTGATA TNTGCCATCA CAGTTGCTAC AATCAGCTCT TTCCAATTTG GCTACCAACA      240
CTGGGGTCAT CAATGCTCCT GAGAAGATCA TAAAGGAATT TATCAATAAA ACTTTGACGG      300
ACAAGGGAAA TGCCCCACCC TCTGAGGTGC TGCTCACGTC TCTCTGGTCC TTGTCTGTGG      360
CCATATNTTC CGTCGGGGGN ATGATCGGCT CCTTTTCCGT CGGACTCTTC GTCAACCGCT      420
TTGGCAGGCG CAATTCAATG CTGATTGTCA ACCTGTTGGC TGTCACCTGGT GGCTGCTTTA      480
TGGGACTGTG TAAAGTAGCT AAGTCGGTTG AAATGCTGAT CCTGGGTCGC TTGGTTATTG      540
ACCTCTTCTG CGGGTCGACG ACCTCTTTGG CCCTCGAGAC A                          581

```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```

GTCAACCTGG GAGGCTCTCC CCCACCTTCT TTCAATCTCT TCTCAAACCTC TGCATCCTCA      60
GAGGGGCCTT GCCTGATTGG CCTTCTTAAA ATGGATCTGC CCCACCCAC TTTGTACTTG      120
CTGTGCCCTC TGCTTTTCAAG CGTGTCTTCA AACAGGATCT CAACAAGGCC TCCCCTGACC      180
ACACTTAAA ACTGCATGCC CTATATATAC CCCATCTCTC TTATTTTAT TTGTCTCCCT      240
AATGCTTATC CCCAGTATAC TCTGTTTATT GTCTGTCTCT CCTCACTACA AAATAAATC      300
CCCAAGGCCT AGAGTTTTTT CTGTCTTGTG CCTGCTATAT ACCAGTGCTT AGAACAGCGC      360
CCTGCACAGA ATAGAGGCC AATTCAATAT GGATTGCTA CCACTACATC CTATTTGTTT      420
CCTTCCCATC ACTTTTCGAA CACTCATCTA TTCAGCTCTG CTGACCTGTT TCACATCTGG      480
ATCCTGTATA GCAACGTCGA CGGCCTCTTT GGCCCTCGAG ACA                          523

```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```

GTNGACTGAT ACTCGAGTAC CTGGATCAGC GGCTGAAAGC TGCAGAGAAC AAGTTTGCCA      60
AGTGCCTCAT GACCTGTCTC AAATGCTGCT TCTGGTGCCT GGAGAAGTTC ATCAAATTCC      120
TTAATAGGAA TGCCTACATC ATGATTGCCA TCTACGGCAC CAATTTCTGC ACCTCGGCCA      180
GGAATGCCCT CTTCCTGCTC ATGAGAAACA TCATCAGAGT GGCTGTCTCT GATAAAGTTA      240
CTGACTTCTT CTTCCTGTTG GGCAAACTTC TGATCGTTGG TAGTGTGGGG ATCCTGGCTT      300
TCTTCTTCTT CACCCACCGT ATCAGGATCG TGCAGGATAC AGCACCACCC CTCAATTATT      360
ACTGGGTTC TATACTGACG GTGATCGTTG GCTCCTACTT GATTGCGTCG ACGGCCTCTT      420
TGGCCCTCGA GACA                          434

```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
GAGGCCCTC AANTTCGCGC ATTTTATTTT ATTTTGTGA NCTGGAGTNT TGCTCTGTAT    60
CCCAGGCTGG AGTGCAGTGG CGCAATCTCG GCTCACTGCA AGNTCCTCCT CCCGGGTTC    120
CGCACATTCT CCTGCCTCAG CCTCCCTAGT AGCTGGGACT ACAGGAGCCC GCCACCACGN    180
CTTGTTAATT TTTTGTGTAT TTTTAGTAGA GACAGGNTTT CACTNTNTTA GTCAGGATGG    240
TCTCATNTT CTGANGTCAT GATCCGCCCA CCTCGGCCTC CCAAAGTGCT GGGAKTACAG    300
GMGCGARCCA CCGCGCCCGG CCTATTTTTT GKGGGTTTNA WWTCTGGGTG ACTGTGCAGC    360
AGGAAGTTTT TGTTKTTTTT TTTCCANTGA AAAGATCTGG CCANAATAGT GGGNNTGTCA    420
AAGTATCTCT TTGCAGNTT AATTTGCATT TTCCANTGA CTAAGATGAT GTTGTGCAAT    480
TTTTTCAGAN ACTGTNTGCT ATCTGTATAT CATCTCTTTT TTTTTTTTC TTTTGGAAGT    540
GGATCCGGTN CGNCCTCTT GCCCTCGAG ACA                                573
```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
GAANCCCCAT CCACTTCNCG GGAGGGGGGA GAGCGCGGNG ACGGGTCTCG CTCCTCGGC    60
CCCGGGATTC GGCGGGTGCA GNTGCCGGAT CCTTCAGCGT CTGNATCTCG GCGTCGCCCC    120
GCGTACCGTC GCCCGGCTCT CCGCCGCTCT CCCGGGGGTT CGGGGCACTT GGGTCCCACA    180
GTCTGGTCCT GCTTCACCTT CCCCTGACCT GAGTAGTCRC CATGGCACAG GTTCTCAGAG    240
GCACTGTGAC TGACTTCCCT GGATTGTATG AGCGGGCTGA TGCAGAACT CTTCGGAAGG    300
CTATGAAAGG CTTGGGCACA GATGAGGAGA GCATCCTGAC TCTGTTGACA TCCCGAAGTA    360
ATGCTCAGCG CCAGGAAATC TCTGCAGCTT TTAAGACTCT GTTGTGCAGG GATCTTCTGG    420
ATGACCTGCG GAAGTGATC CGGTTCCGCC TCTTTGCCCC TCGAGACA                468
```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
GAACCGGATC CACTTCCGGG AAAACCTCGG ATTAGCAAGC AATAAAAACA TGACCTCACT    60
CTTCTCAAA GGAGCCCCTG GTCTCCCTG TGTGACTCAG TTCTTTCCAT CTGTTGTCC    120
CGCTGCAAGC CTCTTCTGC GCTGACTGTG ACATCGGAAC GTGGCCTTCC TGTACCCCC    180
TCCGTGCCAC GCACTGAAGG CCACCCCCC CCACCTGGGA AACTAAGAAC TGGATATTTT    240
GCCTCATTCA CTTGTACTGT AACAAATGTAT ATAATTGGT TGGTATTTC CTATTTAATT    300
TTTAAGAAGC CTATTTTACT AGTGTTTAT ATGAACAAAG TACTGCAGAA GTTAAACCTG    360
```


TGTTGTATTT TTTCTGAGAT GTTTGTCTTT AAGAGATACT TTTTGCTCAG TTTTATATG 420
CCAGGAAGTG GATCCGGTTC GGCCTCTTTG GCCCTCGAGA CA 462

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGCCCCGATNC ACTTCCGTGG NAAGAGCCTG CAATCCCNCC TACTCAGGAG GCTGAGGCAG 60
GAGAATCGCC CGAACCCGAA AGGTGGAGGT TGCAGTGAGC TGAGAATGTG CCACCGCACT 120
CCAGCCTGGG TGACAGGGG AGACTCTCTC AAAGTAAATA AATTAAAAA ATTTAANAAG 180
ATCATCAAAG AACAAACGAA ATTTGTATT TTCAGTAAGT CAATTTAAAC AATAGAAGCC 240
AATTCTACCA CCAGAGGAR CMMATAAAAT CTCATTATTA ATTGAGGGTG GCTTCTCTMC 300
CAGGTGRRAA ATTCTATAGR CAGGTATTTT GKTACTACT GACAGGTAAT AAGATTGTTT 360
CTWAGGTAAA GGTAAACCCA GCAACACAAC ATTCTTCACT TTTGTTTAAT GAACCTCNAN 420
ATTCATCATA TTACTTNTAT TTGCTAGCAT GCTTTTGTG GAAGTGATC CGGTCGGCC 480
TCTTTGGCCC TCGAGACA 498

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

CGASCCGGAT CCACTTCCCC CTTACGTATC ATTTGTCACA CAGGCCTCAG CCGTAAAAA 60
AATTCCAGTT TTTGTGTATT GCAGTTCCCG TATGCTATTG TCAACCAACA GTTCCGTGA 120
TCCTTGAGT CTAATGAGTT TGGATGCATC TATGTTCTTA CTGGATCCAC TGTCCTGCT 180
CGGCAGCTCT TCCTCACTGC TGCTACTCTT TTCTGGACAC TCCTTTTTTT CCATTGTCA 240
AATGTGGTAT TTATGTCTTT ACTGTATCTT TTTTACCCAT GTGAGTTTCA GGAGCCCCAG 300
GGTGCAGGAA GGAGGAGCGG AGGCTTGTG CTGAGCACT GCCAGGCTGC TCTGTGTTCT 360
GTTCTCTTG GRAAGTGGAT CCGGTCGGC CTCTTTGGCC CTCGAGACA 409

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAACCGGATC CACTTCCGAA GAGAAGGTCA GAGCGCACTG CAGGCAGCGC GGCTCTGGGA 60
AGAACTTCAC GGAGCCCCCTT CTTAGAGCAG GGAGGGGGCT TTCTCAGTGA AATGTTTGGT 120

TTTCTGCTGC	CTCCTCTGCC	CCAGGCCCCC	CTCCAGGGTA	CTGCCTATCC	CAGATAGGTC	180
AGTGCACCAG	GGACCCGGCC	GCCAGCACCG	CCGACCCCTC	CCAGAGTGAC	GCCCTTGTTT	240
ACTGACAAAG	AGACCTGTCC	CAGGAGTGTC	CTCCACCGAG	CCGGTCAGCT	GTGGGTGGTT	300
TTCTGTGTAC	GACGCTCAGT	AGCCTGTAGC	AATAACAAAC	TCGTGGCTAT	GAATGCAGAT	360
GCAGTGTCT	CATAGAATAA	CTGTTCTGTC	ACTTTTACAG	ACAAATCTAC	GACAAAAAAA	420
AAGATCAACT	TTTTTTTTCC	GAACAACAAA	AAAAATGAAT	GATTACAATA	GGAAAGGGAA	480
AAATTAAATA	GCTACATATC	ATTAAACAAAT	TAATGTTCTT	CAAAAAATAC	CTACAAATTT	540
CTCTGTACAT	TCTTTACGCA	CAGCGTAACG	ATGGAAGTGG	ATCCGGTTCG	GCCTCTTTGG	600
CCCTCGAGAC	A					611

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAACCGGATN	CACTTCCCCT	CCACGTAGTT	GNAGGGGAA	CCAGCCAACC	CGGCCATAGA	60
TCTCCCCTCG	CCACCAGCCT	TGGTGTCCTT	TCTTGTTAAG	GATCTTGATG	ATGTCACCCT	120
CCTTGAGCGA	CAGCTCTGAT	CGGTCTCGGG	CGCAGAAGTC	ATAGCGGGCT	TTGGGTGTGC	180
CAAAATACTT	TGTGCTTCCC	ACTGNTGGNC	TGCTGATGGT	TCTCTTTTCA	NGCTCCTTGA	240
AGGGGAACCTG	CAANGTGGTG	TCCAGAGACT	TGAAGCAATC	CNTTAGAGAG	TTCTGNTGGT	300
AAAACCTCCAC	CAGNTCCGTA	AGCCCCCNGA	AAGNCTTTTT	CTCTGTGATC	CGGTACAGAA	360
CCTTCTTCTG	TCA					373

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 489 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GTTGACCGCC	CACGATGATC	TTGCCGCCAC	GCTTGCTGGT	CTTCTCCACT	GACAAGGCAC	60
TGCTCAGGCC	CTGCTCATGC	TTCCCCAGAC	CCTGGCCCTC	CCGGAAGCCG	NACTTCTGCA	120
TGATCTTGTTG	CGCCACCGTG	CCCCCATGT	TAGCGAGGAA	GGAGTTGCTA	GGTCCGGTTG	180
GAGATCTCGG	TCTGTCTTGT	TCCTCGTACA	CTGGGGGAGG	AATGGCTGCT	TTGGAAGACT	240
GTGATCGAGG	TCTTGAGTCC	TCTTCATAAG	GAAAATCTCG	GGGTAACCTT	TTGTCTTTCT	300
CTACCAGAGA	AGTGGGTGGG	GCAATGGCAG	CTCCGCCCAT	ACTTCTCTTC	CTCCTCTCTC	360
GCTCATAATC	TTCATCTTCA	TCAGAATCTG	GATCTGGTCT	CCTTGCAAAC	CCACTTGCTT	420
CATGTCTGTC	TTTACGCCTT	TTTCCCTTT	CTTCTATTTC	CGTCGACGGC	CTCTTTGGCC	480
CTCGAGACA						489

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GACGACTTTG	TGGGTATTAA	TTTTGTGTTA	AGTTTAAAAT	AAAAGTAAAG	ATTCATTTTG	60
GATATCAGTT	GAAACCCCTT	AGTAACTCAG	TTTCTGTTAT	TCTTGTTCTC	ATTCCTTTA	120
AATACACTTG	TTCTTGGCTT	TTGCCATTTT	GATTCTGTGA	AGTAGGCAGG	AGCAGGGATT	180
AATTTATACA	GTATTCCTGT	TCTGAACAAA	ACCAGAAAAG	TCACTGTATA	AACTTGACTT	240
AAAATAGTAT	CTTTCTCTTY	TCATGTATTT	TCATTTGGGG	GAAAAAAAAT	CTCTTTAATT	300
GTAACCTGAA	TTCAAGCTGT	ACCCCTCCAT	GGTCCTACAC	TCTAGAGCTA	ATCTGGTTGG	360
GCAGAAAGGC	AGAAGGATGG	TATATTGTCC	CATTGTGCCT	ATAATGTATT	TTAAATTGGT	420
CATTCCACCT	TACCTAATGG	AAATTCTTGC	AGCTTTCCTA	GTGCTCATCA	GCGGTTTAG	480
GAATTCACCTA	ACGTCGACGG	CCTCTTGGC	CCTCGAGACA			520

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTTGACGGCG	TGGTGGCGGG	TGCCTGTAAT	TCCAGCTACT	CAGGAGGCTG	AGGAAGGAGA	60
ATCATTTGAA	CCTGGGAAGT	GGGGGTTGCA	GTGAGCCAAA	ATCGTGCCAT	TGCACTCCAG	120
CCTGGGCAAC	AAGAGTGAAA	CTCCATCTCA	GAAAAAAA	AAAAAAA	AAAAAAAAG	180
GAAGGAACCG	GTGGGGCAAG	CAGAGTTAAG	ATGCTTTGCT	AAGTTAAAA	GTCTACTAAC	240
TACCAAATCT	TGCTGTGGYT	TATCCAGAGC	TCTCAAAATG	CTGCCAATCT	ATTTTAAGA	300
AGACCTAAAT	CCTCATTTG	GCTTTTAGGA	CACTAGGATT	TGCCTTCAAC	CCATGTCTCC	360
AGTCATATAT	TTTCTTACTA	TTCTTCAAC	ATACCTTTTT	CTCTTTTCTT	CACTCTTCAT	420
TATGCTGTTT	AAATCGTCGA	CGGCCTCTTT	GGCCCTCGAG	ACA		463

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GTACAAGAAG	TGGTCCATTC	CTTTGTCTGA	AGGAGCGACA	GGAGCATCTA	CGGTTGAGAA	60
GACAGAAAGT	TTGGCTTCGT	CGATGTCTTG	CTGTGTGAAT	TTTCCAGACT	TAGCCCAGTC	120
GACAGCCTTC	CCAAAAGACT	GGAGCGTCTC	TATTGTATTT	GGGTCCCTGT	AAGAGTAAAC	180
GGTGAAAATC	CCATTGTGGC	TGAGTTTTCG	GCCTCCACCA	TAAGCACCGC	CTTTTCTCG	240
AATTTCTGTA	TGCAAGAATT	TGGCAGTCAT	CAAACGTGCA	AGGATTTTAA	GACTGGCATG	300
ATCTGGGTCC	GTGTAGGGGA	CAGTTCGGAT	GCATTCACCC	ACGTTATTCA	CCGGGAAGGG	360
CATCAGGAAG	TGAGTCTTCA	TCTGCCAGGG	CTTGAAGGTG	GGTTCCATGA	CCAGCTTCCT	420
AATGACCTGG	GAGCCATGGG	GAACGTGGGC	ATCTCCACCA	GAGCTGCTGG	GCACAGGTTT	480
CTCGACCGTG	TGTGGGCGCA	CAGGCCGTCTG	ACGGCCTCTT	TGGCCCTCGA	GACA	534

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 450 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

GTCGACCAGG ACTAGATTCT GTCTCTCCAA AGTGGCCCCA GCCCTGTTCT CTGTACTAGG      60
GAAGCCAGCT GTGTCTTTTC GAGGACAGTT GGTCCAGCCA GCAGGCTCAG TTCAGATACC      120
AGACAACCAT TCCAGCACGA GGGCTCAGCG CCTGGCCCCC GCGGTCGCT CCAGTGCCTG      180
TGTGCCCCACC AGCACATCCA TGAGGTAGTC CAATTCGGCC TCGTCCAGCT CCGGAGCTTC      240
CTCCTTGGCC GGCCCATCCT CAGGGCCTGG TTTGAGGCCC TCAGAGGCTG GTGCCCCAAG      300
TTCATTGTCA TACATAGAGG TGTCAATATC CTCAAACAGG CCCTCAAGCC CATCGTCCAG      360
TAGACAGCCA GTGGCTGGGC CCAGCAGGTC CAAGGCACCC AGGCTGGGCG CTGCTCCCCC      420
GATGCTACGG CCTCTTTGGC CCTCGAGACA      450

```

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 449 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

GTCGACGGCG GYCATGGCAA AGCAGTACGA CTCGGTGGAG TGCCCTTTT TTGTGATGAA      60
GTYTCCCAAA ATACGAAGAA GCTCGCCAAG ATCGGCCAAG GCACCTTCGG GGAGGTGTTT      120
AAGGCCAGGC ACCGCAAGAC CGGCCAGAAG GTGGCTCTGA AGAAGGTGCT GATGGAAGAA      180
GAGAAGGAGG GGTTCCTCAT TACASCCTTG CGGGAGATCA GGATCCTTCA GCTTCTAAAA      240
CACGAGAATG TGGTCAACTT GATTGAGATT TGTCGGAACC AAAGCTTCCC CCTTATAACC      300
GCTGCAAGGG TAGTATWTTA CCTGGTGTTT GACTTCTGCG AGCATGACCT TGCTGGGCTG      360
TTGAGCAATG TTTTGGTCAA GTTCACGCTG TCTGAGATNC AAGAGGGTGA TGCAGATGCT      420
GCTTAACGGC CTCTTTGGCC CTCGAGACA      449

```

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 493 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

GTCGACAAAA CATGGAGTTG TTCCTTTGGC CACATATATG CGAATCTATA AGAAAGGTGA      60
TATTGTAGAC ATCAAGGGAA TGGGTACTGT TCAAAAAGGA ATGCCCCACA AGTGTTACCA      120
TGGCAAAACT GGAAGAGTCT ACAATGTTAC CCAGCATGCT GTTGGCATTG TGTAAACAA      180
ACAAGTTAAG GGCAAGATTG TTGCCAAGAG AATTAAATGTG CGTATTGAGC ACATTAAGCA      240
CTCTAAGAGC CGAGATAGCT TCCTGAAACG TGTGAAGGAA AATGATCAGA AAAAGAAAGA      300
AGCCAAAGAG AAAGGTACCT GGGTTCAACT AAAGCGCCAG CCTGCTCCAC CCAGAGAAGC      360
ACACTTTGTG AGAACCAATG GGAAGGAGCC TGAGCTGCTG GAACCTATTC CCTATGAATT      420

```

CATGGCACAA TAGGTGTTAA AAAAAAAAAA TAAAGGACCT CTGGGGTCAA CGGCCTCTTT 480
GGCCCTCGAG ACA 493

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GTCGACGAGG GGGTCATGGY AGGCAGGGGC AGGTGCGTCA GAGATGGAGC GCAGGTCCTG 60
CATGGAGAAG CTCCGCAGCC TGCCGGCCAG CGCCCCCTGA CTCTTGGTGG CAGCCTGCAC 120
AGCAGCGGAG GCGGCAATGT TGAGGCCCCG CTTCCCGAAG CTGAGCACGG TCTCGTAGCT 180
GCGCTCCTTG GCCTGCACGA TGTACGCGTC GATCTCCTTC TCATGGCGGG ACAGGGACGG 240
GTGGACAAAC TTGCGGTAAA GCAGGCTGGC GCCCTTGGTG TAGGGTGAGA GCAGCCACAG 300
CACGAAGGCC ATCTTGATCT CATAGTAGAA AGGGAACCAG GAGATAAAAA TGTCTGTAAC 360
GATCTCTGCT GCCATGAAGA GTGCARCAA CTATCCAGTA CATCATCCAG TGGACGGCCT 420
CTTTGGCCCT CGAGACA 437

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GTCNACCGCC CTTCTGTCT CCTCCTCAGT NGTACACCTG TGTGGTCTCC ACCACCTCAG 60
ACTTNTCTCCG CCCCTTTCAG TNGGAAGAAG GNGCAGGCC GTCTCGGGT CCTCCACGCA 120
CCGNTCCAGA AGTTGCCTGT ACGTGAGGT CTCATGCGTG TTGGGGTNAA AGAAGCCCTT 180
GGTGTCTGTC CTGGGGTCCG CCGGGACGCG GKTCATCTCC TCACTGAAGT AGCCCCGCTG 240
GTAGRSCAG TCCACAGACA CGCGGTGTT GTGYACGGG TCGATGATRC CGCCCGTGGC 300
GATCTGGGCC TCCAGNAGGN GGATNCCGTG CTGCNGGAGA ACCAGNCCCT TCTNNATGTC 360
CTGGAAGAGN GAGATGGTCC CCCCCAGTA GGGGTCTCTG TANCCGGTGA CGNCCTTCTC 420
GACAGACAGC ATCTGCTCGT GAAGCTCGGG GCCCACCAG CCCGCCTTCA CGGCCTCTTT 480
GGCCCTCGAG ACA 493

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGACCCAC GTTAGTACGG TTGGATAGGA TATGCTCTCA TGGTAACGG TCCAAGTTGG 60

AATGGTCTTC	CAGTCTCCAT	GGNATCCACA	TGCTACTGGC	GTTAGTTCCA	GATCTTGAGG	120
AAGNTATCCC	AGGACCCTGT	CGCCACAGGC	ATGNCATCGT	CANTCACGCC	CAGGCAGCTG	180
ACGCGGTTGT	CATGNCCAGN	CAAGACAAC	GCCCGGTCGG	GTTTGNGTGC	ATCCCAGACG	240
TTGCAGTTGA	AGTCGTCGTA	CCCAGCAAGG	AGGAGGSGSC	CGCTCTTGGW	GAAGGAGACA	300
GAGKTGATCC	CCCAGATGAT	GTTGTCATGG	GAGTAAGTCA	TGAGCTCCYG	GTCAGCACGA	360
AGGTCAAACA	GCCTGCNNGT	GGCGTCGTCT	GAGCCAGTGC	CAAATGCATT	GCCATTTGGA	420
AAGAANCAAA	TGNCATTGAT	GTCAAGACTCG	TGCCCAGTGA	AGGTCTNCCG	GCACATGCCT	480
TCTCGCACAT	CCCAGAGTTT	GTCTGAAGCA	TCACAAGCAC	CAGAGACGAA	CAGTCTGGTG	540
TCAGTCGACG	GCCTCTTTGG	CCCTCGAGAC	A			571

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GTCGACGTAC	CACCAGCAAC	CATCAATCCC	GTCTCCTCCT	GCCTCCTCTC	CTGCAATCCA	60
CCCCGCCACG	ACTATCGCCA	TGGCAGCCCT	GATCGCAGAG	AACTTCCGCT	TCCTGTCACT	120
TTTCTTCAAG	AGCAAGGATG	TGATGATTTT	CAACGGCCTG	GTGGCACTGG	GCACGGTGCG	180
CAGCCAGGAG	CTGTTCTCTG	TGGTGGCCTT	CCACTGCCCC	TGCTCGCCGG	CCCGGAACCTA	240
CCTGTACGGG	CTGGCGGCCA	TCGGCGTGCC	CGCCCTGGTG	CTCTTCATCA	TTGGCATCAT	300
CCTCAACAAC	CACACCTGGA	ACCTCGTGCC	CGAGTGCCAG	CACCGGAGGA	CCAAGAAGCTG	360
CTCCGCCGCC	CCCACCTTCC	TCCTTCTAAG	CTCCATCCTG	GGACGTGCGG	CTGTGGCCCC	420
TGTCACTGG	TCTGTCTCT	CCCTGCTGCG	TGGTGAGGCT	TATGTCTGTG	CTCTCAGTGA	480
GTTCTGTGGAC	CCTTCTCTAC	TCACGGCCTC	TTTGGCCCTC	GAGACA		526

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 520 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTGACTTTG	TGGGTATTAA	TTTTTGTTTA	AGTTTAAAT	AAAAGTAAAG	ATTCAATTTG	60
GATATCAGTT	GAAACCCCTT	AGTAACTCAG	TTTCTGTTAT	TCTTGTTCTC	ATTTCCCTTTA	120
AATACACTTG	TTCTTGCTT	TTGCCATTTT	GATTCTGTGA	AGTAGGCAGG	AGCAGGGATT	180
AATTTATACA	GTATTCCTGT	TCTGAACAAA	ACCAGAAAAG	TCAGTGTATA	AACTTGACTT	240
AAAATAGTAT	CTTCTCTTTT	TCATGTATTT	TCATTTGGGG	GAAAAAAAT	CTCTTTAATT	300
GTAACCTGAA	TTCAAGCTGT	ACCCCTCCAT	GGTCTACAC	TCTAGAGCTA	ATCTGGTTGG	360
GCAGAAAGGC	AGAAGGATGG	TATATTGTCC	CATTGTGCCT	ATAATGTATT	TTAAATTGGT	420
CATTCCACCT	TACCTAATGG	AAATTCTTGC	AGCTTTCCTA	GTGCTCATCA	GCGGTTTTAG	480
GAATTCACTA	ACGTCGACGG	CCTCTTTGGC	CCTCGAGACA			520

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

GAATTCGGCC AAAGAGGCCG TTGACGGGGC TGGAGGAGGA AGAAGAGGTG GATCCCCGGA      60
TCCAGGGAGA ACTGGAGAAG TTAAATCAGT CCACGGATGA TATCAACAGA CGGGAGACTG      120
AACTTGAGGA TGCTCGTCAG AAGTTCCGCT CTGTTCTGGT TGAAGCAACG GTGAAACTGG      180
ATGAACTGGT GAAGAAAATT GGCAAAGCTG TGGAAGACTC CAAGCCCTAC TGGGATGCAC      240
GGAGGGTGGC GAGGCAGGCT CAGCTGGAAG CTCAGAAAGC CACGCAGGAC CTCCAGAGGG      300
CCACAGAGGT GCTCCGCGCC GCCAAGGAGA CCATCTCCCT GGCCGAGCAG CGGCTGCTGG      360
AGGATGACAA GCGGCAGTTC GACTCCGCCT GGCAGGAGAT GCTGAATCTC GCCACTCAGA      420
GGGTCATGGA GCGCGAGCAG ACCAAGACCA GGAGCGAGCT GGTGCATAAG GAGGTCGACG      480
GCCTCTTTGG CCCTCGAGAC A                                     501

```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

GTCGACCGTG TCCAGAGCCC ACCTCCCTCA CACCCACACA GCGCTTCCTA AAGGCAGGGA      60
CAGGAGCTGG CCTCCCTCGC CTGCTGGCAT GGGGCTGGAC ACAGGAGGAA GTGGCGTGGG      120
GGCTGCCTGA GGGGAGTGAG GCGGCAGGAT AGCTTCCCCA GCAGGTCTCT GGCTCAGGTC      180
CAGGTATCTC CTCCTCCCCA TACCTCTGCC TCTCGCCTCC GCTCAGAAAA GCAGGTGCCC      240
TTAAGAGCCA TCTCCACCCC CATGTAAACT GCACACAGGA AGGGAGAGGC CACTCCGACT      300
GCTCTGAGGT CCAGGTAGGA TGGTTTCCCC CAGTGTCTGG GTGGGGAGCA AGGAACTCCA      360
GGGGCGACCT TGTGCCACCG CATCACCTTC CTGCTCAGGG AAGGGGCCCG TGCTGCCGCT      420
TGGAGGGTGC CATGCCCAGA GCCTCTGCCC CTAGCCTCAG CCTCGCCTAC TCCTGGGGGG      480
CTCCAGCACC CCCGGCCGTC AACGGCCTCT TTGGCCCTCG AGACA                     525

```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

GTCGACGCGA GTGGAGACCT GTGGTAGAGA AGCTCCTTTT GATGTCCTAC AGGCTTTCCA      60
CTGTGGTGTC TCCAGTCATT CAGAGCTCAT CCCCTGAAGG CCTCATCCCA ATGGACACTG      120
ATTGAGAGTC AGCAASCCGC TTACAGATGA TTCTGAATGA GATTCANCCT CGAGATACTA      180
ATGATTATTT TAACCAAGCC AAAATATTGA AAGAACATGA TAGCTTTGAT ATGAAGGACT      240
TGAATGCTAG TGTGGTGAAT ATTGATACTT CTACAGAAAT CAAAGGTAAA GAAGTAAAAA      300
CATGTGATGT AACTGCGCAG ATGGTGCTGG TATGTTGTTG GAGAAGTATG AAGGAAGTTG      360
CTTTACTTTT AGGCATGTTG TGCCAGCTTC TGCCCATGTC AACGGCCTCT TTGGCCCTCG      420
AGACA                                     425

```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

GGGACGTAAT CAACCCAAGC TTATGACCCG CACTTACTGG GAANTCNTCG TTCATGGGGA      60
AGAANTGCAA TCCCCGATCC GCCATCACGA ATGGGGGGCA CCGGGTTANC CGCGCCTCCC      120
GGCGTAGGGT AGNCACACNC TGANNCAGTC AGTGTATCGC GCGTGCATCN CCGGACATCT      180
AAGGGCATCA CAGACCTGTT NTTGNTCAAT CTCGGGTGGN TGNNCGCCAC TTGTCNCTCT      240
AAGAANATGG GGGACGCCGC CCNCTCGGGG GTNGCGTAAC TAGNTAGNAT NCCAGAGTCT      300
CGTTCGTTAT CGGAAGTAAC CAGACANATC GCTCCCCCAN CTAAGANNNG CCATNCACCA      360
CCACCCACGG AATCGAGANA GAGCTATCAA TCTGTTGTTA GGACATGCCC GGCTTGCTTG      420
GTCATCATCT TGGTGACNC GACCTCTTTG NCCCTCGAGA CA                        462

```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

GTCGACAGAA ATCATTATTC TTTATTTGCA GNCATTCCAC CCCACCTATG TTTTCTTCTC      60
CTTCCTTCTT CTCTGTCAGG AGAGTTCTTG TCATGCTGAG CTTCTTCATT GTATGGCATT      120
TATATTTTAG CACTGTTTTA TTATTGCTT CTGTATCAGC ATGTTCAACA TTTTCTTCAA      180
ATATAACACA GGTCCCTAGA GTGTCTTCAT ACTCCCCAGC AAAGACACAG CTGTCCACTT      240
GCAGAATGGG CCTCTCAGTG TCAATGCCCA AAACCTTGCA TTTATTTTCA CATTTTGAGA      300
GGAAGTCTGA ATCAATAATT CCTGATAATT CCACCAGAAC CAACTGCTCC TCCTCTTCCT      360
CGTCTTCTCC GTCCTCTGGA CTCCGCTCGT CCGCCGCCGC CGCCATGGTC CCGCGGCGGT      420
TGACGGCCTC TTTGGCCCTC GAGACA                        446

```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

GANTTCCAGT GAAGTTGCCT TTTTGCCNNC CCTAGNCATC CAACCTINTCN AAAACCAAGT      60
ANACNAGGCT GATTCTGGAA GTTCTTGAGG AAAAAGCAAG CTTTACAACC AAAATACCCA      120
GATGCTGTGN CCACATGGCT AAACCCTTGA CCCATCTCAG AAGCAGAATC TCCTANCCCC      180
ACAGAGTGCT GTGTCCTCTG AAGAAACCAA TGACTTTAAA CAAGAGACCC TNCCAAGTAA      240
GTCCANCGAA AGCCATGACC ACATGGATGA TATGGATGAT GAAGATGATG ATGACCATGT      300

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GGACAGCCAG GACTCCATTG ACTCCGACGA CTCTGATGAT CTAGATGACA CTGATGATTC	360
TCACCACTCT GATGAGTCTC ACCATTCTGA TGAATCTGAT GAACCGGTCA CTGATTTTCC	420
CACGGACCTG CCANCAACGT CGACGNCCTC TTTGNCCTC GAGACA	466

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GTCGACAGCG ACCGCTCCTC CCTTCCTTCC TTGAATCAGA GCACGGTAGA AAGCTGCTGC	60
TCTATGCCGA AGTGTTCGGA AATTCTTGGC AGCTGCATAG ACCGCGGGGC TGTCCCCTAA	120
CCTTTGCTCT TGTGCGCTCC TCCACCAGGA GGGCCCCCT CCCTGTACCC CAGCTTCCCA	180
CAGAGCTGCA GGCACAGCTT GGCTGCCTCC CGCTTCCAGA CCCCTATCTC CATCAGGTGG	240
GCCTGAGGCG GGGCTGACTC TTTCTTTAGG CCCCTCACAG GGACTAGAGC AGAATGGCAC	300
TCAGTAAGCA GGGGTGACAA CTAGAGGAAT GGCAGGGTGT GTTCAGCTGG GAGAACAGTT	360
ACCAGAGACG CTGTGATTCT TCAGGTGTGA GGGCAACTGT TACAAGACTT AAGTAGCAAC	420
AACAACCATG GTAGACGCTG CCTTCGATTG TGCCCTTGGG AGTCCCAGGC CTGGCACCAG	480
GCCCTACTCA TCCTTCATTT CTTTTCTTT TCTTTGTTT TTTGTTTTT GGGTTTTTG	540
GTCAACGGCC TCTTGGCCC TCGAGACA	568

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATTCANTTT GGATATCAAG TTGNCNCCCC CNTAGTAACT CAGTTTCTGT TATTCTTGTT	60
CTCANCTTCC CNATAAAAAC ACTTGTTCTG GGTNTTGCC ANNTTGATTC TGTGAAGTAG	120
GCAGGAGCAG GGATTAATTN ATANAGTATT CCTGTTCTGA NCGCAACCAG AAAAGTCACT	180
GTATAAACTT GACTTAAAAT AGTATCTNTC TCTTTTCATG TATANTCAGG TGGGGGGGNA	240
AAAATCTCTT TAATTGTAAC CTGAANTCAA GCTGTACCCC NCCATGGTCC TACACTCTAG	300
AGCTAATCTG GNTGGGCAGA AAGGCAGAAG GATGGTATAT TGTCCCATG TGCCTATAAT	360
GTATNTTAAA NTGGTCATTC CACCTTACCT AATGGAAATT CTTGCAGCTT TCCTAGTGCT	420
CATCAGCGGT TTTAGGAAGT CACTAACGTC GACGCGCTCT TTGGCCCTCG AGACA	475

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```

CCTGAGTTGT GTCTAAGGNN CNCAAGACAA GTACCCAAGT TTCCTCTAGN TTTCTCTTT      60
AAGCTTCTCN AGTCATACAT TTNCAAGCGT CCTTTTGTCA ACCATNCCAG TCNANATACA      120
TTATTTGTCC TCCAATGGNT GACTTGCCAG CATCTACGTG NCCAATGAAT ACTACATTTA      180
CATGCTCTTT CTTAGGAGCA CTTGGCGGTG CAACCACAGA CTTAGGTNTT GGGATTTCTT      240
CTTCCTCCTC CATCATTTC TGGGCACTTT TCTCTGGCGG CTTTCCATCT CCCAAGGAAC      300
CACCCCTGG CTCTGCTTCA CTTATTTCTT CTTTGTGCTC CCATGATTCT TCTGGAGACA      360
TTTCTGTCTC TCCACTTTCT ACAATAGGTT CTGAAAGTTC CATGCTAACA GCTGAATTTG      420
AACCTTCACA CAATGACTGT TCGTCGACGG CCTCTTGGC CCTCGAGACA      470

```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```

GAATTCGGCC AAAGAGGCCT ACTCACAGTC ATCAATTATA GACCCACAA CATGCGCCCT      60
GAAGACAGAA TGTTCATAT CAGAGCTGTG ATCTTGAGAG CCCTCTCCTT GGCTTTCCTG      120
CTGAGTCTCC GAGGAGCTGG GGCCATCAAG GCGGACCATG TGTCAACTTA TGCCCGGTTT      180
GTACAGACCC ATAGACCAAC AGGGGAGTTT ATGTTTGAAT TTGATGAAGA TGAGCAGTTC      240
TATGTGGATC TGGATAAAAA GGAGACCGTC TGGCATCTGG AGGAGTTTGG CCGAGCCTTT      300
TCCTTTGAGG CTCAGGGCGG GCTGGCTAAC ATTGCTATAT TGAACAACAA CTTGAATACC      360
TTGATCCAGC GTTCCAACCA CACTCAGGCC GTCGAG      396

```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```

GAATTCGGCC AAAGAGGCCT ACCCGATTGC TAAATGGATT ATGAAAGCAA ATTGCTACTG      60
GGAGGTGATG GTCAAAAGCA AACTTAGATG GTTTTCACAC CATCTGTCAT CATGACTCAA      120
AGGGAAATGC TAGCCACACC ATTTTCCAGT GAAGCCACTG CTTTACACAG TAGATACACA      180
TAGCTTCCTA TTGTTATTTT CTTTCTAAT TATGTACATT TAGAAAAAAA ATACAACACT      240
GTGTAAACA GCAGGACAGC TAGCAATGGA ACATACAACA CTATGCTGAA AAACCACAAC      300
AGCTTGGTTA AGCGGAGGAG AGAAACAGAG ATGGCCTTCA TGGAGTGAAG CTGTCAATGC      360
CTGCCATCTC CTTAGTCTGT GACGGATCTG CACTCTGAGG GCAGGCCTTC TGAGCGCCGC      420
CACTTTGCCA GCGCTGCTT AAACCATTTT TGGGTCTCCT CCTCGGAAAG GCCTGCCTCG      480
GCCGCGATGA GGCACAGCGT GGTGGAATCC GGGTGCTTGT CGAG      524

```

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GAATTCGGCC AAAGAGGCCT ATTTTTTTTT TCTTTTTTTA GGCATATGTA GTAATATTAG	60
AAACATTTAA TTTGGGAAAC TTTGATTCTT GAAAGAGAAA ACAAAGCAT GTGAATAAAC	120
TTTGAAGTGT TCACCTCAGT TTGGGACCAA ACTGCTTGGA TCTTTGTAAA AACCGGTTTT	180
GTATGTCAA GAGGAGTTTA AGGCCTTTCC GACCACCTG TGTTCCTT TTCTGCCAG	240
CCATGTATCA CGTGGAGTTG CTCCTTACCA CACCTCACGT GCCCCTGAGC CCTATTTCCT	300
GATTCTTCT GGGCTGGACT TCCCCGTTCT CCACCAGCAG CTCCAGTATC CCTGTTGAAT	360
TCTAGACCTG CGTCGAG	377

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAATTCGGCC AAAGAGGCCT AGCGGACAAG TTTGAGAGAC CTGGCCTTGG CCAAAGCCCT	60
CGATTCGCTG TGTCAGAAAA ACTGAGGTGA GAAGAGACCA CCACCCTCTC CACCACCCTC	120
TCAGTAGGAA AGCGGGATCA ACAGAGATCA GAAGGACAGC ACACTCACAC CTGCACATGA	180
ACACACCATC TATGTCAGGA AATCCAGGGG AAGGGGAAGA GGGGTGGAGT GGCTCCGCAG	240
GGCTGACCTG ACAGGGGACA GGAACACTCC CTTAGACCCA GGAAGTCGC CCCAAATCCA	300
AAGCTCTTGA AAGGAGGTAT GGCCTCGAAA CTCCAGAAGC CTCTTCTGCC AACGCACCGA	360
GGACCTGCAC CTCCCATTC A GCACGCGTCG AG	392

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CAATTCGGCC AAAGAGGCCT ACAGCATTTT TACTCCTTCC AAGAAGAGCA GCAAAGCTGA	60
AGTAGCAGCA GCAGCACCAG CAGCAACAGC AAAAAACAAA CATGAGTGTG AAGGGCATGG	120
CTATAGCCTT GGCTGTGATA TTGTGTGCTA CAGTTGTTCA AGGCTTCCCC ATGTTCAAAA	180
GAGGACGCTG TCTTTGCATA GGCCCTGGGG TAAAAGCAGT GAAAGTGGCA GATATTGAGA	240
AAGCCTCCAT AATGTACCCA AGTAACAACT GTGACAAAAT AGAAGTGATT ATTACCCTGA	300
AAGAAAATAA AGGACAACGA TGCCTAAATC CCAAAGTCGA G	341

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAATTCGGCC AAAGAGGCCT AGCAGTAGCA TGTGCAGCAA CCAATCAAGA TGGAGAACTA	60
TACCTGCACT CATTGTGTG TTTGCATGTA TAGTTCTCTG CAGTAGCATG TGCAGCAACC	120
AATCAAGATG GAGAACTGTT CCATCGCAAA GCTCCCTCTT GCCACTTCTT TTTAGCCACC	180
CAATCCTCTC TGCTCCCGTC GAG	203

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAATTCGGCC AAAGAGGCCT ATGAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC	60
TTTGGACCTG ATCAGCTTGA TACAAGAACT ACTGATTTCA ACTTCTTTGG CTTAATTCTC	120
TCGGAAACGA TGAAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTTGGGT	180
TCTCTTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT	240
TTTAATGCAG GTCATTCAGA TGTAGCGGAT AATGGAACTC TTTTCTTAGG CATTTTGAAG	300
AATTGGAAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTC	360
AAACTTTTTA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTGGA GACCATCAAG	420
GAAGACATGA ATGTCAAGTT TTTCAATAGC AACAAAAAGA AACGAGATGA CTTCGAAAAG	480
CTGACTAATT ATTCGGTAAC TGACTTGAAT GTCCAACGCA AAGCAATACA TGAATCATC	540
CAAGTGATGG CTGAACTGTC GCCAGCAGCT AAAACAGGGG TCGAG	585

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCGGCC AAAGAGGCCT ACTGGCGGCC GCGGAGACGC AGAGTCTTGA GCAGCGCGGC	60
AGGCACCATG TTCCTGACTG CGCTCCTCTG GCGCGGCCGC ATTCCCGGCC GTCAGTGGAT	120
CGGGAAGCAC CGGCGGCCGC GGTTCGTGTC GTTGCCCGCC AAGCAGAACA TGATCCGCCN	180
CCTGGAGATC GAGGCGGAGA ACCATTACTG GCTGAGCATG CCCTACATGA CCCGGGAGCA	240
GGAGCGCGGC CAGCGCGCGG TGCGCAGGAG GGAGGCCTTC GAGGCCATAA AGGCGGCCGC	300
CACTTCCAAG TCCCCCGCGC ATAGATTCAT TGCGGACCAG CTCGACCATC TCAATGTCGA	360
G	361

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAATTCGGCC AAAGAGGCCT AAACAAATG GTTATCAACC ACTTGGAGAA GTTGTTTGTG	60
ACAAACGATG CAGCAACTAT TTTAAGAGAA CTAGAAGTAC AGCATCCTGC TGCAAAAATG	120
ATTGTAATGG CTTCTCATAT GCAAGAGCAA GAAGTTGGAG ATGGCACAAA CTTTGTCTG	180
GTATTTGCTG GAGCTCTCCT GGAATTAGCT GAAGAACTTC TGAGGATTGG CCTGTCAGTT	240
TCAGAGGTCA TAGAAGGTTA TGAAATAGCC TGCAGAAAAG CTCATGAGAT TCTTCCTAAT	300
TTGGTATGTT GTTCTGCAAA AAACCTTCGA GATATTGATG AAGTCTCATC TCTACTTCGT	360
ACCTCCATAA TGAGTAAACA ATATGGTAAT GAAGTATTC TGGCCAAGCT TATTGCTCAG	420
GCATGTCGAG	430

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCGGCC AAAGAGGCCT AGAAGAAGAT GATCCTAAAC AAAGCTCTGA TGCTGGGGGC	60
CCTCGCCCTG ACCACCGTGA TGAGCCCTTG TGGAGGTGAA GACATTGTGG CTGACCACGT	120
TGCCTCTTAC GGTGTAAACT TGTACCAGTC TTACGGTCCC TCTGGCCAGT TCACCCATGA	180
ATTTGATGGA GACGAGGAGT TCTATGTGGA CCTGGAGAGG AAGGAGACTG TCTGGAAGTT	240
GCCTCTGTTC CACAGACTTA GATTTGACCC GCAATTTGCA CTGACAAACA TCGCTGTGCT	300
AAAACATAAC TTGAACATCC TGATTAAACG CTCCAACCTCT ACCGCTGCTA CCAATGAGGT	360
TCCTGAGGTC GAG	373

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCGGCC AAAGAGGCCT ACTTAACCAG AATGACAGTC TTTCCCTAT CTTCTTCTT	60
TATTCTTATC TTCTATCTTT CCCTCCCAA CTCTTTCCCC GACATAACAG AAAACATGAA	120
GGAATTAAAG GAGGCCAGGC CGCGCAAAGA TAACAGGCGT CCAGATCTGG AAATCTATAA	180
GCCTGGCCTT TCTCGGCTAA GGAACAAGCC CAAAATCAAG GAACCCCTG GGAGTGAGGA	240
ATTCAAAGAT GAAATTGTTA ATGACCGAGA TTGCTCTGCT GTTGAAAATG GTACACAGCC	300
CGTCGAG	307

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GGAGCTGCAC ATGGTACTTT TGGAGAGCCT GGTGGAAATC ATTTTGGTTG CTGTTTCAGCA	60
TGTGGATTAT AGTCTTCGAT GTGAGCAGGA TCCAGAGAAG AAAGCTTTTA TCAGACAGAA	120
TGCATCCTTT TTATATGAAA CAGTCCTCCC TGTGGTGGAG AAAAGGTTTG AAGAAGGTGT	180
GGGGAAACCT GCCAAGCAAC TCCAAGATCT GAGGAATGCA TCTAGACTTA TTCGTGTGAA	240
TCCTGAAGTC GAG	253

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAATTCGGCC AAAGAGGCCT ACACATATTG GAAAAATGAT CTTTTTGGAG CACTGTTCTG	60
CTGCTTAGAC CCAGTACTCA CTATTGCTGC TAGTCTCAGT TTCAAAGATC CCATTTGTCA	120
TTCCACTGGG AAAAGAAAAG ATTGCAGATG CAAGAAGAAA GGAATTGGCA AAGGATACTA	180
GAAGTGATCA CTTAACAGTT GTGAATGCGT TTGAGGGCTG GGAAGAGGCT AGGCGACGTG	240
GTTTCAGATA CGAAAAGGAC TATTGCTGGG AATATTTTCT GTCTTCAAAC ACACTGCAGA	300
TGCTGCATAA CATGAAAGGA CAGTTTGCTG AGCATCTTCT TGGAGCTGGA TTTGTAAGCA	360
GTAGAAATCC TAAAGATCCA GAATCTAATA TAAATTCAGA TAATGAGAAG ATAATTAAAG	420
CTGTCGAG	428

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCGGCC AAAGAGGCCT ACAAGACGTC ATTTCACAAA GTGCGCCATT CTGAGGATAT	60
GCAGTTTGCC TTCTCTTATT TTTATTATCT CATGAGTGCA GTGCAGCCAC TGAATATATC	120
TCAAGTCTTT GATGAAGTTG ATACAGATCA ATCTGGTGTC TTGTCTGACA GAGAAATCCG	180
AACACTGGCT ACCAGAATTC ACGAACTGCC GTTAAGTTTG CAGGATTGA CAGGTCTGGA	240
ACACATGCTA ATAAATTGCT CAAAAATGCT TCCTGCTGAT ATCACGCAGC TAAATAATAT	300
TCCACCAACT CAGGAATCCT ACTATGATCC CAACCTGCCA CCGGTCCTA AAAGTCTAGT	360
AACAACTGT AAACCAAGTA CTGACAAAAT CCACAAAGCA TATAAGGACA AAAACAAATA	420
TAGGTTTGAA ATCATGGGAG AAGAAGAAAT CGCTTTTAAA ATGATTTCGT CCAACGTTTC	480
TCATGTGGTT GGCCAGTTGG ATGACATAAG AAAAAACCCT GTCGAG	526

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GGGTGGCAAT ATGGA	CTCC	TCTTTCTGC	CANCCCANAC	CCATACATCG	GGATTCTAT	60
AATACCTTCG TTGGTCTCCC	TAACATGTAG	GTGGNGGNGG	GGAGATATAC	AATAGAACAG		120
ATACCAGACA AGACATAATG	GGCTAAACAA	GACTACACCA	ATTACACTGC	CTCATTGATG		180
GTGGNACATA ACGAGCTAAT	ACTGTAGCCC	TAGACTTGAT	AGCCATCATC	ATATCGAAGT		240
TTCACTACCC TTTTCCATT	TGCCATCTAT	TGAAGTAATA	ATAGGCGCAT	GCAACTTCTT		300
TTCTTTTTTT TTCTTTTCTC	TCTCCCCCGT	TGTTGTCGAG				340

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCGGCC AAAGAGGCCT	ACGTCCTTTT	AAATCTTAAT	GAAATATCAT	GGAATATTGT	60
ATGGTCTTCA TATCGTTCTA	TATAATGCAA	ATGGTGAAC	GCTCTGTCT	TTGCTTTCCT	120
GAAAGCATCC ATCCGATCAG	TAGCTTTCCC	AATAGAAAAA	CCTGCAGCTC	CTTTTCCGTT	180
CCCCACAGCC ACCAAGACAC	GGATCGATTT	CTTCTTCCC	TCTTTCGAG	TCATAGTGAA	240
AACGTTTCTT ACCTCAAGTA	TCCTGGTATC	AAAATCCTCA	TATGTTTCTC	CACAGTCGAG	300

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTCGGCC AAAGAGGCCT	ACCAGCTTTG	AGGTTGACCT	GTTTCTCTTT	GTCTGCCTTC	60
CCAAAACACC AGCCCCAGG	AAGACATTAA	GCAGCCTTAA	GCTTAAATTC	CTACTCCCTC	120
TTCCAAATTT GGCTCACTTG	CCTTAGATCC	AAGGCAGGGA	AAGGAAAAGA	AGGGGGGTCT	180
CTGGCTTTAT TACTCCCTA	AGTCTTTACT	CTGACTTCCC	CAAACCCAGA	AAGATTTTCT	240
CCACACTGTT CATTTGAAAG	AGGAGTATTT	TGTCCCATTT	TCCCCTTCCT	CATTATCAAA	300
CAGCCCCAGT CTTCTTGTC	TCTGCTAAGA	AAGTAGAGGC	ATGATGATCT	GCCTCTCAAC	360
TGCCCTAGTC GAG					373

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 644 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GAATTCGGCC	AAAGAGGCCT	ACGCAGATAC	GGGCTTACAG	ATACTTTTTA	CACTCTTACA	60
AAATGTTGCA	CAAGAAGAAG	CTGCAGCTCA	GAGTTTTTAT	CAAACCTTAT	TTTGTGATAT	120
TCTCCAGCAT	ATCTTTTCTG	TTGTGACAGA	CACTTCACAT	ACTGCTGGTT	TAACAATGCA	180
TGCATCAATT	CTTGCAATATA	TGTTTAATTT	GGTTGAAGAA	GGAAAAATAA	GTACATCATT	240
AAATCCTGGA	AATCCAGTTA	ACAACCAAAT	CTTCTTCAG	AAATATGTGG	CTAATCTCCT	300
TAAGTCGGCC	TTCCCTCACC	TACAAGATGC	TCAAGTAAAG	CTCTTTGTGA	CAGGGCTTTT	360
CAGCTTAAAT	CAAGATATTC	CTGCTTTCAA	GGAACATTTA	AGAGATTTCC	TAGTTCAAAT	420
AAAGGAATTT	GCAGGTGAAG	ACACTTCTGA	TTGTTTTTTG	GAAGAGAGAG	AAATAGCCCT	480
ACGGCAGGCT	GATGAAGAGA	AACATAAACG	TCAAAATGTCT	GTCCCTGGCA	TC'TTAAATCC	540
ACATGAGATT	CCAGAAGAAA	TGTGTGATTA	AAATCCAAAT	TCATGCTGTT	TTTTTTCTCT	600
GCAACTCGTT	AGCAGAGGAA	AACAGCATGT	GGGTATTTGT	CGAG		644

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAATTCGGCC	AAAGAGGCCT	ACGTTATACT	ATTAGATCCT	TTCATTATCA	ATCCCTTTTA	60
AAGGCAAGGA	AACAGGTTCA	GCAAGATCAG	CTGACTTCTC	TGTGTAAGTG	GGACCTGAGA	120
TTTGAAAGTT	GAGAGCAGCA	TGTTTTGCCC	ACTGAAACTC	ATCCTGCTGC	CAGTGTTACT	180
GGATTATTCC	TTGGGCCTGA	ATGACTTGAA	TGTTTCCCCG	CCTGAGCTAA	CAGTCCATGT	240
GGGTGATTCA	GCTCTGATGG	GATGTGTTTT	CCAGAGCACA	GAAGACAAAT	GTATATTCAA	300
GATAGACTGG	ACTCTGTCAC	CAGGAGAGCA	CGCCAAGGAC	GAATATGTGC	TATACTATTA	360
CTCCAATCTC	AGTGTGCCTA	TTGGGCGCTT	CCAGAACCGC	GTACACTTGA	TGGGGGACAA	420
CTTATGCAAT	GATGGCTCTC	TCCTGCTCCA	AGATGTGCAA	GATGTGAG		469

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAATTCGGCC	AAAGAGGCCT	AGAGGGGACT	CGCCGCCATC	TCAGGTCTCT	TGGCTTTGCC	60
AGGGCCCACC	GGAGAAACT	GACGACCCGT	TTCTGTAATC	CTTATGGGAG	ACCAACCTTG	120
TGCCTCCGGG	AGATCCACTC	TCCCACCTGG	AAACGCACGG	GAAGCCAAGC	CTCCAAAAAA	180
GCGCTGCCTC	CTCGCTCCGC	GTTGGGATTA	TCCGGAAGGA	ACTCCCAACG	GAGGTAGTAC	240
CACTCTACCC	TCCGCACCTC	CTCCTGCATC	AGCCGGCCTG	AAGTCGCACC	CTCCTCCTCC	300
GGAGAAGTAG	AGAAATAAAT	TTCTCCCACC	CTAAACCACT	CTTTGAGTGA	TGTCAGTATG	360
ACTCCATTTT	CCTGGTGCAT	TCATATAATA	GTTACCTGG	TGAAAACAAT	GAAGATTATT	420
TACAATGCTA	CCCCG					435

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
GAATTCGGCC AAAGAGGCCT AACCAAGCAG AAGCTGTACC ACAAGAAGAT CTTCCGGACT    60
GCCATGCTGT TCCAGTTTGT GAACGTGCTG CTCCAGGTCC TGGTCCACAA GTCCCATGAT    120
CTTCTGCAGG AGGAGATTGG CATCGCCATC TACAACATGG CCTCAGTCGA G              171
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
GAATTCGGCC AAAGAGGCCT AGTCATGACT CCCCTGATTG GGCTCCTAAT GTCACTTATT    60
CCCTGCCCAG AACCAAAAGT GGTAAGCCC CAGAAAGAGC CTCTAGCAAG ACTTCTCCAC    120
ATTGGAAGGA GTCAGGAGCC TCCCATTGT CATTCCTAAA GAACAGCAAA TATGAGTATG    180
ACCCTGACAT CTCTCTCCA CGAAAAAGC AAGCAAAATC CCATTTTGA GACAAGAAGC    240
AGCTTGATTG CAAAGGTGAC TGCCAGAAAG CAACTGATTC AGACCTTTCT TCTCCACGGC    300
ATAAACAAAG TCCAGGGCAC CAGGATTCTG ATTCAGATCT GTCACCTCCA CGGAATAGAC    360
CTAGACACCG GG                                372
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
GAATTCGGCC NAAGAGGCCT AGGGTGGGAC AAGAGAGTGA GACTAGAATA TAAATATCCG    60
TAAACAGCAT CTGAGCATTG GTCTTTAACA GGGAGGAGGA ACCACTGGTG TATATTAATT    120
TAGGACACAG GATCATTATA GGGGTNGGGC CAGCTGGTGT TAATGGCATG CAGGCATATG    180
TGATGCCAAC CATGAGGGCT GGAAGAACCA GAAGCCAAAG AAGAATATGA CCGCATCTAT    240
TCTAAAGCTA CTGTGGTGGT TTCTCATGCT TCAGAGTCTC GTAAGTCTCC TGGTTCCTGG    300
TGCTCAGGCC CGTGTAACA CCATCTGATT TCTCATAGCT GGTATAGCT GCCTTCGCA      360
CTTGATCTT CAGTCGAG                        378
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
GAATTCGGCC AAAGAGGCCT AGGTGCCGCG GTCCTGTCTT GCTGTGCCTG CGGCAGGGGC      60
TCGGAACCAA TTCATTCCCTG CACGGCCTGG GGCAGGAGCC CTCGAGGGA GCTCGGTCAC      120
TGTGTTGCAG GTCCTCGCCT AGAGACCTGC GAGATGGAGA AAGAGAGCAC GAGGCGGCAC      180
AAAGGAAAGC CCCAGGAGCA GAGTCTTGCC CATCTCTCCC TCTGAGCATC TCGGACATTG      240
GGACTGGATG TCTTTCGTCA CTGGAAAACC TCAGACTGCC GACGCTGCCG GAAGAGTCAT      300
CCCCTCGAGA GCTCGAGGAC TCGAGCGGAG ACCAGGGCCG GTGCGGTCCC ACACACCAGG      360
GATCCGAGGA TCCTTCGATG CTCTCGCAGG CCCAGTCCGC TACCGAGGGT CGAG          414
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
AAGCGTGCTC GTGCCCCGTAT TNCCNAGGGG NTCAGTCTGT NNCGCCCANA GNCCAAGNCC      60
AAGCCCCAAGN CCNAGNCCAA GGATCCANNC CAAGGCCCCAG GCTGCAGCCC CAGCTTCAGT      120
TCCAGCTCAG GCTCCACAC GTACCCAGGC CCCACAAAG GCTTCAGAGN AGATATCTCT      180
CCCAACATGA GGACAGAAGG ACTGGTGCGA CCCCCACCC CCGCCCCTGG GCTACCATCT      240
GCATGGGGCT GGGTCCTCCT GTGCTATTG TACAAATAAA CCTGAGGCAG TCGAG          295
```

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
ATGGACTTCC TCTTTTCTGC CANCCACAC CCATACATCG GGAGCCTATA ATACCCTTCG      60
TTGNTCTCCC TAACATGTAG GTGGCGGAGG GGAGATATAC AATAGAACAG ATACCAGACA      120
AGACATAATG GGCNNAACAA GACNACACCA ATTACNCTNC CTCATTGATG GTGGNACATA      180
ACGAGCTAAT ACTGTANCCC TAGACNTGAT AGCCATCATC ATATCGAAGT TTCCTACCC      240
TTTTTCCATT TGCCATCTAT TGAAGTAATA ATAGGCGCAT GCAACTTCTT TTCTTTTTTT      300
TTCTTTTCTC TCTCCCCCGN TGTGTCTCA CCATATCCGC AATGACGTCG AG          352
```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAATTCGGCC	AAAGAGGCCT	ACGTTATCCG	CGATGCGTTT	CCTGGCAGCT	ACATTCCTGC	60
TCCTGGCGCT	CAGCACCGCT	GCCCAGGCCG	AACCGGTGCA	GTTCAAGGAC	TGCGGTTCTG	120
TGGATGGAGT	TATAAAGGAA	GTGAATGTGA	GCCCATGCCC	CACCCAACCC	TGCCAGCTGA	180
GCAAAGGACA	GTCTTACAGC	GTCAATGTCA	CCTTCACCAG	CAATATTCAG	TCTAAAAGCA	240
GCAAAGCCGT	GGTGCATGGC	ATCCTGATGG	GCGTCCAGT	TCCCTTCCCC	ATTCTTGAGC	300
CTGATGGTTG	TAAGAGTGGA	ATTAAGTCC	CTATCCAAAA	AGACGTCGAG		350

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GAATTCGGCC	AAAGAGGCCT	ATTGAATTCT	AGACCTGCGT	CGACCTCCCT	TCCAGCCCCC	60
AGAAAGCTCG	GTCACTTGAG	TGTTTCTAG	AATCCTGGGG	TGCTCCCGGG	CCGCTCTCAG	120
AGAAGTGGCA	GGTTTCACGT	TCAGCCGTGT	GGCGGATCGT	GTGGCTTCCA	AAGCCTTTTA	180
CAGCCCCCGC	CCCCATCCC	GTGGTCTGTC	TGCAGGAACT	CTCCCGTCTG	TGAGAAGCCT	240
CTTTCCGAGT	CGAG					254

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCGGCC	AAAGAGGCCT	ACTAGAGGGG	TCAGTGGCCC	CGCACGGTGG	GGTGGCCGCT	60
CAGGGCCTAG	GGAGCAGGTG	GGAGGGGCTT	GGAGGGCAGA	ACAGAGGGCC	TGGGGGCTGC	120
TCTGCTGGCC	ACCACTGCTT	TCTGGTTGAA	CCAGATAAGT	AGCTGGTGGT	GACGGCTGTG	180
GGCCCTGAGT	CGGGGGAGAA	GAGGCAGAGG	GAGCAGTGGG	CTGGGCTAGT	GGGGACATGA	240
GTGGGTGGTG	ATCATGCCTG	TGTCGGGGGA	GCTGAGGCAG	AGAGTGGGGC	AGCGAGCATC	300
CCCTGAGGGC	AGGAGGAGAG	GGGTGGGGAC	AGGGAAGGGT	CGGGGGTGGT	CCCAGCCCTG	360
AAGACAGGAG	TGGCGAGGGC	AGGTGTGCTC	TAGGTGCTTG	TCGAGGTGGA	CAACATGGGT	420
CGAG						424

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCGGCC	AAAGAGGCCT	AATGGCGTCC	AGGTCTAAGC	GGCGTGCCGT	GGAAAGTGGG	60
GTTCCGCAGC	CGCCGGATCC	CCCAGTCCAG	CGCGACGAGG	AAGAGGAAAA	AGAAGTCGAA	120
AATGAGGATG	AAGACGATGA	TGACAGTGAC	AAGGAAAAGG	ATGAAGAGGA	CGAGGTCATT	180
GACGAGGAAG	TGAATATTCA	ATTTGAAGCT	TATTCCTAT	CAGATAATGA	TTATGACGGA	240
ATTAAGAAAT	TACTGCAGCA	GCTTTTTCTA	AAGGCTCCTG	TGAACACTGC	AGAACTAACA	300
GATCTCTTAA	TTCAACAGAA	CCATATTGGG	AGTGTGATTA	AGCAAACGGA	TGTTTCAGAA	360
GACAGCAATG	ATGATATGGA	TGAAGATGAG	GTTTTTGTT	TCATAAGCCT	TTTAAATTTA	420
ACTGAAAGAA	AGGGTACCCA	GTGTGTTGAA	CAAATTCAG	AGTTGGTTCT	ACGCTTCTGT	480
GAGAAGAACT	GTGAAAAGAG	CATGGTTGAA	CAGCTGGACA	AGTTTTTAAA	TGACACCACC	540
AAGCCTGTGG	GCCTTCTCCT	AAGTGAAAGA	TTCATTAAATG	TCCCTCCACA	GATCGCTCTG	600
CCCATGTACC	AGCAGCTTCA	GAAAGAACTG	TCGGGGGCAC	ACAGAACCAA	TAAGCCATGT	660
GGAAGTGCT	ACTTTTACCT	TCTGATTAGT	AAGACATTTG	TCGAG		705

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAATTCGGCC	AAAGAGGCCT	ACCCAGCTCA	GAATCTTGCT	GCTCGGCCCC	CAGGAGAGCA	60
ACAACACAAC	GGGAACGATG	TGGAAGGTGT	CAGCTCTGCT	CTTCGTTTTG	GGAAGCGCGT	120
CGCTCTGGGT	CCTGGCAGAA	GGAGCCAGCA	CAGGCCAGCC	AGAAGATGAC	ACTGAGACTA	180
CAGGTTTGGA	AGGCGGCGTT	GCCATGCCAG	GTGCCGAAGA	TGATGTGGTG	ACTCCAGGAA	240
CCAGCGAAGA	CCGCTATAAG	TCTGGCTTGA	CAACTCTGGT	GGCAACAAGT	GTCAACAGTG	300
TAACAGGCAT	TCGCATCGAG	GATCTGCCAA	CTTCAGAAAG	CCCAGTCGAG		350

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GAATTCGGCC	AAAGAGGCCT	AGTGGACAGG	AAGTAGAATT	TATTGGTGAG	TATTAAGAGG	60
GGGGCAGCAC	ATTGGAAGCC	CTCATGAGTG	CAGGGCCCGT	CACTTGTCCA	GAGGGCCACG	120
ACTGGGGATG	TACTTGACCC	CACAGCCATC	TGGGATGAGC	CGCTTTTCAG	CCACCATGTC	180
TTCAAATTCA	TCAGCATTGA	ACTTGGTGAA	GCCCCACTTC	TTGAGATGT	GGATCTTCTG	240
GCGGCCAGGA	AAC TTGAACT	TGGCCCTGCG	CAGGGCCTCA	ATCACATGCT	CCTTGTTCTG	300
CAGCTTGGTG	CGGATGGACA	TGATAACTTG	GCCAATGTGA	ACCCTGGCCA	CAGTGCCCTG	360
GGGCTTTCCA	AAGGCACCTC	GCATGCCTGT	TTGGAGCCTG	TCAGCCCCAG	CACAGGACAA	420
CATCTTGTG	ATGCGGATGA	CGTGTCGAG				450

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 585 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
GAATTCGGCC AAAGAGGCCT ATGAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC      60
TTTGGACCTG ATCAGCTTGA TACAAGAACT ACTGATTTCA ACTTCTTTGG CTTAATTCTC      120
TCGGAAACGA TGAATATATC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTTGGGT      180
TCTCTTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT      240
TTTAATGCAG GTCATTCAGA TGTAGCGGAT AATGGAAGTC TTTTCTTAGG CATTTTGAAG      300
AATTGGAAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTTC      360
AAACTTTTTA AAAAATTAA AGATGACCAG AGCATCCAAA AGAGTGTGGA GACCATCAAG      420
GAAGACATGA ATGTCAAGTT TTTCAATAGC AACAAAAAGA AACGAGATGA CTTCGAAAAG      480
CTGACTAATT ATTCGGTAAC TGACTTGAAT GTCCAACGCA AAGCAATACA TGAATCATC      540
CAAGTGNTGG CTGAAGTGTG GCCAGCAGCT AAAACAGGGG TCGAG                        585
```

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
GAATTCGGCC AAAGAGGCCT ATTGGAGTTT GAGTATAGTA AATTATGATC CTTAAATATT      60
TGAGAGTCAG GATGAAGCAG ATCTGCTGTA GACTTTTCAG ATGAAATTGT TCATTCTCGT      120
AACCTCCATA TTTTCAGGAT TTTTGAAGCT GTTGACCTTT TCATGTTGAT TATTTTAAAT      180
TGTGTGAAAT AGTATAAAAA TCATTGGTGT TCATTATTTG CTTGTCCTGA GCTCAGATCA      240
AAATGTTTGA AGAAAGGAAC TTTATTTTTC CAAGTTACGT ACAGTTTTTA TGCTTGAGAT      300
ATTTCAACAT GTTATGTATA TTGGAAGTTC TACAGCTTGA TGCCTCCTGC TTTTATAGCA      360
GTTTATGGGG AGTCACTTGA AAGAGCGTGT GTACATGTAT TTTTCTCTN GGCAAACATT      420
GAATGCAAAC GTGTATTTT TTAATATAAA TATATAACTT CCTGCGTCCA G                        471
```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```
GAATTCGGCC AAAGAGGCCT ATGTTTGGCA ACTGGGGTGA AGGGATTGCC CTCCCCCTGC      60
TGGGATCCCC CCAGCCCCTC CGGTCTGGCA GGAAGGGGGC AGCCTGCAAC CCCCAGGGC      120
AGGTGTGGGG CTGCCAGATG CTCCAGGCAG GGGGCCAGAA GGGGCTCACA AAGGCTTGCC      180
CTCCAGGGAG ATGACGGCAC TGCCCCCAG CTTCTCTGCC AGGGTGCAAG GGTCTTGAG      240
CTCCTCGTAG CAGTTTGCTT GCAATTCATG CTTGATCCCT GTCAGCTTCT TCTTGATGGC      300
GTCCTTGGAG CTGGCATAAA TCATTTTGCT CTTAAGGGGS GCAGACTCGG GGGCCCAGAA      360
GATAAACACC AGATCCTCCT TCTTGCTCTC CYTGGTCTCA TAGGTTGCAT CATAGAGGGC      420
```

ATAGCGGCAG TCCTTATCTG GCAGCATCTT GACAAAGGTG GCGTAGGGAT CGTCGAG

477

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GAATTCGGCC CAAAGAGGCC YMAAAGATCA GCTATTAGAA GAGAAAGATC AGTTAAGTCC	60
TTTGGACTTG ATCAGCTTGA TACAAGAACT ACTGATTTC ACTTCTTTGG CTTAATTCTC	120
TCGGAACCGA TGAAATATAC AAGTTATATC TTGGCTTTTC AGCTCTGCAT CGTTTGGGT	180
TCTCTTGGCT GTTACTGCCA GGACCCATAT GTAAAAGAAG CAGAAAACCT TAAGAAATAT	240
TTTAATGCAG GTCATTGAGA TGTAGCGGAT AATGGAACTC TTTTCTTAGG CATTTTGAAG	300
AATTGGAAAG AGGAGAGTGA CAGAAAAATA ATGCAGAGCC AAATTGTCTC CTTTACTTC	360
AAACTTTTAA AAAACTTTAA AGATGACCAG AGCATCCAAA AGAGTGTCTGA G	411

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GAATCGGCCC AAAGAGGCCT ACTGAAGATC AGCTATTAGA AGAGAAAGAT CAGTTAAGTC	60
CTTTGGACCT GATCAGCTTG ATACAAGAAC TACTGATTTC AACTTCTTTG GCTTAATTCT	120
CTCGGAAACG ATGAAATATA CAAGTTATAT CTTGGCTTTT CAGCTCTGCA TCGTTTGGG	180
TTCTCTTGGC TGTTACTGCC AGGACCCATA TGTAAGAGAA GCAGAAAACC TTAAGAAATA	240
TTTAATGCA GGTCAATCAG ATGTAGCGGA TAATGGAAC TTTTCTTAG GCATTTTGAA	300
GAATTGGAAA GAGGAGAGTG ACAGAAAAAT AATGCAGAGC CAAATTGTCT CTTTACTT	360
CAAACTTTT AAAAATTTA AAGATGACCA GAGCATCCAA AAGAGTGTGG AGACCATCAA	420
GGTCGAG	427

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAATTCGGCC AAAGAGGCCT AGAGAAGATA AACTGGACA CTGGGGAGAC ACAACTTCAT	60
GCTGCGTGGG ATCTCCAGC TACCTGCAGT GGCCACCATG TCTTGGGTCC TGCTGCCTGT	120
ACTTTGGCTC ATTGTTCAAA CTCAAGCAAT AGCCATAAAG CAAACACCTG AATTAACGCT	180
CCATGAAATA GTTTGTCCTA AAAAATTCA CATTTTACAC AAAAGAGAGA TCAAGAACAA	240

CCAGACAGAA AAGCATGGCA AAGAGGAAAG GTATGAACCT GAAGTTCAAT ATCAGATGAT	300
CTTAAATGGA GAAGAAATCA TTCTCTCCCT AAAAAAACC AAGCACCTCC TGGGGCCAGA	360
CTACACTGAA ACATTGTACT CACCCAGAGG AGAGGAAATT ACCACGAAAC CTGAGAACAT	420
GGAACTACTGT TACTATAAAG GAAACATCCT AAATGAAAAG AATTCTGTG CCAGCATCAG	480
TACTTGTGNC GGGTTGAGAG GATACTTCAC ACATCATCAC CAAAGATACC AGATAAAACC	540
TCTGAAAAGC ACAGACGAGA AAGAACATGC CGTCTTTACA TCTAACCAGG AGGTCGAG	598

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAATTCGGCC AAAGAGGCCT AGAGCTAAGG CGAAGACCAA GACACGTGAC ATTCATGCTT	60
TGGTGTGGGG TCCAAAGCAC TCTTATTAA CATAGATTCC AAACCTTTTA CACCCATGGG	120
GTACATATA CTCTTTATTT TACCCTTCAT TATTTTAAAA ATCACAACAT CACCCATTGC	180
CCCCGTGTCC AAAGGAATCG CTTGTAATAA ATCAGCAGGT CTAGAATTCA ATCGGGAG	238

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GAATTCGGCC AAAGAGGCCT AGAGCTAAGG CGAAGACCAA GACACGTGAC ATTCATGCTT	60
TGGTGTGGGG TCCAAAGCAC TCTTATTAA CATAGATTCC AAACCTTTTA CACCCATGGG	120
GTACATATA CTCTTTATTT TACCCTTCAT TATTTTAAAA ATCACAACAT CACCCATTGC	180
CCCCGTGTCC AAAGGATTCC CTTGTAATAA ATCAGCAGGT CTAGAATTCA ATCGGGAGGT	240
TCTCCCTATA GTGAGTCGTA TTAATTCAG AGGAGTATT AGAAGAGAAG CTGAAGCTGT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GAATTCGGCC AAAGAGGCCT ACGACAGTTG GTGTAAAGGA AAACCTCTGA GCTCCGTGAG	60
TTCACCTGGT ACATTGGAAT TAAAGTGCTT GGATGTTTTT CCCCCACTTT AAAAAAACTT	120
TTGAGGTTTT TTTTTTTTTT TGCTTTTAA AAACATCGTA ACATTAACAC ATGGCCGTTC	180
ACCGTCCCCC AGCGATGGGA GCTGGCCTGG GGCCAGGGT CCTCCAGGAT CTCACTCAT	240

TCACAGTAAC GGTCTGACC AGTCCTCCAG GTCGCACGTG GATGCGACAG GGGTGGGGAG	300
GGAGGAGGAA GTGACTGTCC CACCTCTGCA GGACCATGGG AGTGGGCAAG GTCTTCTCCG	360
GGGCGCACCC CTGAACCCAG GGGTGCTGCA GGACNTG	397

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 592 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GAATTCGGCC AAAGAGGCCT ATAAGAATTT AAGATGCATT TTTGCATTG CTATATTTCT	60
TTAAATTCTA GATAGTTATT TTCAAGTGTT GGTAAACATA AATCTTAGGC TTAGGAACCA	120
TTGGATTAGT AACAGCATTG TGCTAATCAA AACTTTAAAA AAATGAGTTC AAAATTGTGA	180
TAATGTAATT TTATAGATT TCTTTTATCC TCAACCTGCA GAAGCCGAA AGTGAGGCAC	240
ATAGCCCCAC ATAGGCAGAA ATTAAGCCT AGGCAATAAC TTAGTGAAAA TGGAAATTTTC	300
AGAACATTCC ACTTCTTGT TAGTACAATT TTATGGCCAT GGTGCTAGCT AATGGAAATG	360
GCTAGTATAC TATTATAGG CCAGCAATAT TTTGGTGAAT TTAAGCGAAA CTATGCTCAG	420
TATCATTGAA ATGGGGGTGG GGTGGGCTTG AGACATGAAA TCAATCATAC AAAGTCAAAA	480
ACTATTTTAA CCCAGGAATA AGTTAAATTC CTGTCACCCA GTCGAGGTTC TCCCTATAGT	540
GAGTCGTATT AATTTCAGAG GAGTATTTAG AAGAGAAGCT GAAGCTGTCT AG	592

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAATTCGGCC AAAGAGGCCT AGATGATGAT ATGTTTAAACC ACCAAGTTCC TTATTGTGG	60
CTGATTTACT GCCTTGTCA TCCTCTCAA TCAAGTATTA AAGAAACAGT GGAGGCATAT	120
GAGGCAGCAT TAGGGGTGGC TATGAGATGT GATATAGTAC AGAAGATATG GATGGATTAT	180
CTTGCTTTTG CAAATAATAG AGCTGCTGGA TCCAGAAACA AAGTTCAGA ATTCAAATTT	240
TTTACTGATT TAGTGAATAG ATGTTTGTT ACAGNCCCTG CCCGATACCC CATTCTTTT	300
AGCAGNGCTG ATTACTGGTC CAACTATGAA TTTCATAATA GGGTCGAG	348

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAATTCGGCC AAAGAGGCCT ACAGAATTGA GASTTTGTTT TTACACACAA GTTTAATGCC	60
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ACCTTCCTCT	GTCTGCCATG	GACCAACAAG	CAATATATGC	TGAGTTAAAC	TTACCCACAG	120
ACTCAGGCCC	AGAAAGTTCT	TCACCTTCAT	CTCTTCCTCG	GGATGTCTGT	CAGGGTTCAC	180
CTTGGCATCA	ATTGCCCCTG	AACTTAGCT	GTGCTGGGAT	TATTCTCCTT	GTCTTGGTTG	240
TTACTGGGTT	GAGTGTTTCA	GTGACATCCT	TAATACAGAA	ATCATCAATA	GAAAAATGCA	300
GTGTGGACAT	TCAACAGAGC	AGGAATAAAA	CAACAGAGAG	ACCGGGTCTC	TTAAACTGCC	360
CAATATATTG	GCAGCAACTC	CGAGTCGAGG	TTCTCCCTAT	AGTGAGTCGT	ATTAATTTCA	420
GAGGAGTATT	TAGAAGAGAA	GCTGAAGCTG	TCGAG			455

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCGGCC	AAAGAGGCCT	AAAAATCTCT	TATTAAAGGT	AGAACCTCTG	CTAGCCAGAC	60
AACTATATTA	TTTGCTCAA	CAAAACAGTG	GACATTTCTT	GAGGGGCTAC	GATTACCAG	120
AACACATCAG	CAATCCAGAA	GATTACCACA	GATCTATCCG	CCATTCCTCT	ATCAAGAAT	180
GAAAAATGTC	AAGATGAGTG	GTTTTCTTTT	TCCTTTTTTT	TTTTTTTTTT	TTTGATACG	240
GGGATACGGG	GTCTTGCTCT	GTCTCCAGG	CTGGAGTGCA	GTGACACAAT	CTCAGCTCAC	300
TGTGACCTCC	GCCTCCTGGG	TTCAAGAGAC	TCTCTGCCT	CAGTCGAG		348

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAATTCGGCC	AAAGAGGCCT	ACCTTAAAGC	CGTATACTTA	TGAATTTAAA	GTGGAAAATT	60
TTTTTGGTGG	CCCTGGCCCC	CTTGCCAGAT	TCCAGCTGGC	CGTCAGTGCT	CGCGTGTCTC	120
TCTGAAGAGG	CTCTGCGGTT	CTGGTCCCTG	TGCCTGAGCT	CCAGGTGCCG	CCAGACATTA	180
TACAACGTGA	AGGCTGAGAT	CTTTCCCCCT	TCGGGAATGG	AGTATTGCAG	AACAGGCTCC	240
CTCTGCTCCC	TGGAGGTTTT	GATCACGAGG	CTCTCAGACC	TCTTGGAGGT	GGATAAAGAT	300
GAAGCACTGA	CTGAATCTGA	TGAGCATTTT	TCGACAAAGC	TTATGTATGA	AGTTGTCGAG	360

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GAATTCGGCC	AAAGAGGCCT	ACTCATCTTG	GGTCCCAGCC	AGGCCCCCCC	AAAACCAAAG	60
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CCCCTTCAAG	TCCTGGGGTC	CCAGCCTGTG	CCCCCAGCTT	CCTGCCCACC	CAGCCCCGAG	120
CATTCTCACA	CAGAGAAAGA	ACAAGCAAGG	GCTCCAGGGG	GACAGGATGG	GGCAGGGCAT	180
ACAGTGGGGG	GTGGGGGGGC	AGCTGGGAGG	AGGGAGGGAC	AAAACAAAAC	ATTTTCCTTT	240
GGGTTTTTTT	TTTCTTTCTT	TTTTCTCCCC	TTTACTCTTT	GGGTGGTGTT	GCTTTTCCTT	300
TCCTTTTCCC	TTTGAGATTT	TTTTGTGTGTT	GTTCCTTTT	TGTATTTTAC	TGATATCACC	360
AGGATAGTTT	ACTCTCCTTC	TAGCTTTCTG	CTTACCGCAC	ACTGGATAAC	ACACACATAC	420
ACACCCACAA	AAATGCTCAT	GAACCCAATC	CGGAGAAGGT	TCCAGCAGGT	CCCCCACCTT	480
CCCCCTCTCC	TCCTACTTCT	CCTCTTGACA	GCGAGGACAG	GAGGGGGACA	AGGGGACACC	540
TGGGCAGACC	CGCCGGCTCT	CCCCCACCC	CACCCGTCG	AG		582

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCGGCC	AAAGAGGCCT	AGAAATAAAA	CATTCTACAC	CGTCTCCTAC	CAAATATTCA	60
CTATCACCAA	GTAAAAGTTA	CAAGGTAAAC	AGGAAAGAAT	GGAATCATTT	CATTGTGAAA	120
TTGTTTCTGT	TCTAAGTGT	TTAAATGCTG	TTTTGTTATT	TTTATTTTT	TTTTCAGTAT	180
TCTCCCGAAA	CACCACCTCG	ATGGACAGAA	GATCGGAATT	CTTTACTGAA	TATGATTGTC	240
CAACAAGTAG	AGGCCATGTC	GAG				263

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCGGCC	AAAGAGGCCT	AATTTCTCAG	CTCCAAGCAT	TAGGTAAACC	CACCAAGCAA	60
TCCTAGCCTG	TGATGGCGTT	TGACGTCAGC	TGCTTCTTTT	GGGTGGTGCT	GTTTTCTGCC	120
GGCTGTAAAG	TCATCACCTC	CTGGGATCAG	ATGTGCATTG	AGAAAGAAGC	CAACAAAACA	180
TATAACTGTG	AAAATTTAGG	TCTCAGTGAA	ATCCCTGACA	CTCTACCAAA	CACAACAGAA	240
TTTTTGGAAT	TCAGCTTTAA	TTTTTTGCCT	ACAATTCACA	ATAGAACCTT	CAGCAGACTC	300
ATGAATCTTA	CCTTTTGGGA	TTTAACTAGG	TGCCAGATTA	ACTGGATACA	TGAAGACACT	360
TTTCAAAGCC	ATCATCAATT	AAGCACACTT	GTGTTANCTG	GAAATCCCCT	GATATTCATG	420
GCAGAAACAT	CGCTTAATGG	GCCCAAGTCA	CTGAAGCATC	TTTCTTAAT	CCANNCGGGA	480
ATATCCAATC	TCGAGTTTAT	TCCAGTGCAC	AATCTGGAAA	ACTTGAAAG	CTTGTATCTT	540
GGAAGCAACG	TCGAG					555

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAATTCGCCC	AAAGAGGCCT	AGATGATGAT	ATGTTTAAAC	ACCAAGTTCC	TTATTTGTGG	60
CTGATTTACT	GCCTTTGTCA	TCCTCTTCAA	TCAAGTATTA	AAGAAACAGT	GGAGGCATAT	120
GAGGCAGCAT	TAGGGGTGGC	TATGAGATGT	GATATAGTAC	AGAAGATATG	GATGGATTAT	180
CTTGTCTTTG	CAAATAATAG	AGCTGCTGGA	TCCAGAAACA	AAGTTCAAGA	ATTCAAATTT	240
TTTACTGATT	TAGTGAATAG	ATGTTTGTTT	ACAGNCCCTG	CCCGATACCC	CATTCTTTT	300
AGCAGNGCTG	ATTACTGGTC	CAACTATGAA	TTTCATAATA	GGGTCGAGGT	TCTCCCTATA	360
GTGAGTCGTA	TTAATTCAG	AGGAGTATTT	AGAAGAGAAG	CTGAAGCTGT	CGAG	414

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 590 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCGGCC	NAAGAGGCCT	AAGCAGATGC	TGATCTCATT	ATGCTTGGCC	TTGCCACACA	60
TGAACCGAAC	TTTACCATT	TTAGAGAAGA	ATTCAAACCA	AACAAGCCCA	AACCATGTGG	120
TCTTTGTAAT	CAGTTTGGAC	ATGAGGTCAA	AGATTGTGAA	GGTTTGCCAA	GAGAAAAGAA	180
GGGAAAGCAT	GATGAACTTG	CCGATAGTCT	TCCTTGTGCA	GAAGGAGAGT	TTATCTTCCT	240
TCGGCTTAAT	GTTCTTCGTG	AGTATTTGGA	AAGAGAACTC	ACAATGGCCA	GCCTACCATT	300
CACATTTGAT	GTTGAGAGGA	GCATTGATGA	CTGGGTTTTT	ATGTGCTTCT	TTGTGGGAAA	360
TGACTTCCTC	CCTCATTGTC	CATCGTTAGA	GATTAGGGAA	AATGCAATTG	ACCGTTTGGT	420
TAACATATAC	AAAAATGTGG	TACACAAAAC	TGGGGGTTAC	CTTACAGAAA	GTGGTTATGT	480
CAATCTGCAA	AGAGTACAGA	TGATCATGTT	AGCAGTTGGT	GAAGTTGAGG	ATAGCATTTT	540
TAAAAAGAGA	AAGGATGATG	AGGACAGTTT	TAGAAGACGA	CAGGGTCGAG		590

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GAATTCGGCC	AAAGAGGCCT	AGACGGGCCT	CGGTCAGCAG	CACGGGGTGC	TCCTCGGGAG	60
CCACACGCAG	CTCATTGTAG	AAGGTGTGGT	GCCAGATTTT	CTCCATGTCG	TCCCAGTTGG	120
TGACGATGCC	GTGCTCGATG	GGGTACTTCA	GGGTGAGGAT	GCCTCTCTTG	CTCTGGGCCT	180
CGTCGCCCAC	ATAGGAATCC	TTCTGACCCA	TGCCCAACAT	CACGCCCTGG	TGCTGGGGC	240
GCCCCACGAT	GGAGGGGAAG	ACGGCCCGGG	GGGCATCGTC	CCCCGCGAAG	CCGGCCTTGC	300
ACATGCCGGA	GCCGTTGTCTG	AG				322

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

GGGTGACAA ATATGGACTT CCTCTTTTCT GCCNNCCCAA ACCCATACAT CGGGATTCCT      60
ATAATACCTT CGTTGGTCTC CCTAACATGT AGGTGGCGGA GGGGAGATAT ACAATAGANC      120
AAGATACCAG ACAAGACATA ATGGGCTAAA CAAGACTACA CCAATTACAC TGCCTCATTG      180
ATGGTGGTAC ATAACGAACT AATACTGTAG CCCTAGACTT GATAGCCATC ATCATATCGA      240
AGTTTCACTA CCCTTTTTC ATTTGCCATC TATTGAAGTA ATAATAGGCG CATGCAACTT      300
CTTTTCTTTT TTTTCTTTT CTCTCTCCCC CGTTGTTGTC TCACCATAG      349

```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

GAATTCGGCC AAAGAGGCCT ACTATAAGAG AGATCCAGCT TGCCTCCTCT TGAGCAGTCA      60
GCAACAGGGT CCCGTCCTTG ACACCTCAGC CTCTACAGGA CTGAGAAGAA GTAAAACCGT      120
TTGCTGGGGC TGGCCTGACT CACCAGCTGC CATGCAGCAG CCCTTCAATT ACCCATATCC      180
CCAGATCTAC TGGGTGGACA GCAGTGCCAG CTCTCCCTGG GCCCCTCCAG GCACAGTTCT      240
TCCCTGTCCA ACCTCTGTGC CCAGAAGGCC TGGTCAAAGG AGGCCACCAC CACCACCGCC      300
ACCGCCACCA CTACCACCTC CGCCGCCGCC GCCACCACTG CCTCCACTAC CGCTGCCACC      360
CCTGAAGAAG AGAGGGAACC ACAGCACAGG CTTGTGTCTC CTTGTGATGT TTTTCATGGT      420
TCTGGTTGCC TTGGTAGGAT TGGGCCTGGG GATGTTTCAG CTCTTCCACC TACAGAAGGA      480
GCTGGCAGAA CTCGAGAGT CTACCAGCCA GATGCACACA GCATCATCTT TGGAGAAGCA      540
AATAGGCCAC CCCAGTCCAC CCCCTGAAAA AAAGGAGCTG AGGAAAGTGG CCCATTTAAC      600
AGGCAAGTCC AACGTCGAGG TTCTCCCTAT AGTGAGTCGT ATTAATTTCA GAGGAGTATT      660
TAGAAGAGAA GCTGAAGCTG TCGAGACA      688

```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

GAATTCGGCC AAAGAGGCCT AATGATTTTG ATAGGAAGAA TGTCAGCCCA GGTTCCTCATG      60
AACATGACCA TCACAGGTTG TATGATGACG TTTTACAGGA CTACGCCGGC TGTGCTGTTG      120
TGGCAGTGGA TTAACAGTC CTTCAATGCC GTCGTCAATT ACACCAACAA AAGTGTGCGAG      180

```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```

GAATTCGGNC AAAGAGGCCT ACCACCTTCT CTGCCAGAAG ATACCATTTC AACTTTAACA      60
CAGCATGATC GAAACATACA ACCAACTTC TCCCCGATCT GCGGCCACTG GACTGCCCAT      120
CAGCATGAAA ATTTTATGT ATTTACTTAC TGTTTTCCTT ATCACCAGA TGATTGGGTC      180
AGCACTTTTT GGTGTGTATC TTCATAGAAG GTTGGNCAAG ATAGAAGATG AAAGGRAWYY      240
TYMATKRARR WTTTKKKWTY MWKRAACSR WWCARRRRW KSMAMMMRG RRRRRRRWCC      300
YYWWYCYTWC YTKRWSYTKK KRRGRRRTW AAARCCMRKT TKGWRGGSYT TKKKRWGRW      360
TTWTWWKKTW AAMMAMRRRG RRRMSRCGR RARRAAAMMR CYTTTGNAAT NCNCCNAGGT      420
GATCAGAATC CTCACATTGC GGCACATGTC ATAAGTGAGG CCANCAGTAA AACAACATCT      480
GTGTTACAGT GGGCTGANAA AGGATACTAC ACCATGAGCA ACAACTTGGT AACCTGGAA      540
AATGGGAAAC AGCTGNCCGT TAAAAGACAA GGACTCTATT ATATCTATGC CCAAGTCGAG      600

```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

```

NCCTGTTTCA TTAATTAAAT TTCCCGAAAG AACCTGAGTC ATTTTCCNAC ATGAGAATAC      60
TAGAAGAATG ACCAAGACTT GCGAGACGCG ATTTNCCGGG TGGTGCGAAC AATAGANCGA      120
CCATGACCTT GAAGGTGAGA CGCGCATAAC CGCTAGAGTA CTTTGAAGAG GAAACANCAA      180
TAGGTTGCTA CCAGTATAAA TAGACAGGTA CATACAACAC TGGAAATGGT TGTCTGTTG      240
AGTACGCTTT CAATTCATTT GGGTGTGCAC TTTATTATGT TACAATATGG AAGGGAACCT      300
TACACTTCTC CTATGCACAT ATATTAATTA AAGTCCAATG CTAGTAGAGA AG              352

```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```

GAATTCGGCC AAAGAGGCCT AAAGAAGACA AAGATGATAG GCGGCACAGA GATGACAAAA      60
GAGATTCCAA GAAAGAGAAA AAACACAGTA GAAGCAGAAG CAGAGAAAGG AAACACAGAA      120
GTAGGAGTCG AAGTAGAAAT GCAGGGAAAC GAAGTAGAAG TAGAAGCAAA GAGAAATCAA      180
GTAACATAAA AAATGAAAGT AAAGAAAAAT CAAATAAACG AAGTCGAAGT GGCAGTCAAG      240
GAAGAACTGA CAGTGTTGAA AAATCAAAAA AACGGGAACA TAGTCCCAGC AAAGAAAAAT      300
CTAGAAAGCG TAGTAGAAGC AAAGAACGTT CCCACAAACG AGATCACAGT GATAGTAAGG      360
ACCAGTCAGA CAAACATGAC CGTCGAG              387

```

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GAATTCGGCC	AAAGAGGCCT	AAGGAAGTTG	GATGTTTTGA	TTTACTGTT	TATAGATGTT	60
AGATTGTACA	GATTTGCTG	TATTTCTCAC	CATATCTAAT	GATACTTTTT	TCATTAGATT	120
GGTCTTCAAG	AACAGTATTA	GTTATAATTA	TTTTGGTTAT	TCAGTATATA	GTTAGCTCTT	180
ACAGTTTAGC	TTTATTCACC	ATATTTATAC	TGTGGATTCA	CAGCGAGAGG	TAGAGGTTAT	240
TCCAGGAGAG	TTGATGACCT	TCATTTAAAG	TCCAATAAAA	ATCAGTAGTA	GAAACATAAG	300
AAAACATCTT	TGCAATATTT	ACTTTTGTTT	CTGTTTGCCG	TAAATAGTAA	CATTGTTTTT	360
TTTTATTTTG	TGTTTGTAT	AAAACAGTTG	CATTCACAAT	ATTATTGGCC	TGAGATATTG	420
ATGATATTGT	GATGGTATGA	AAATGTGTAC	ATTCCCTGTG	CAACATCAGA	TTTGCAGGAA	480
AAATGAAGCA	CTTACTGAAA	TCGCTGGTAC	TCGTCGAG			518

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAATTCGGCC	AAAGAGGCCT	AGGACAAAAC	AAAACATTTT	CCTTTGGGTT	TTTTTTTCT	60
TTCTTTTTTC	TCCCCTTTAC	TCCTTGGGTG	GTGTTGCTTT	TCCTTTCCTT	TTCCCTTTGA	120
GATTTTTTTC	TTGTTGTTTC	CTTTTGTAT	TTTACTGATA	TCACCAGGAT	AGTTTACTCT	180
CCTTCTAGCT	TTCTGCTTAC	CGCACACTGG	ATAACACACA	CATACACACC	CACAAAATG	240
CTCATGAACC	CAATCCGGAG	AAGGTTCCAG	CAGGTCCCCC	ACCCTCCCCT	CCTCCTCCTA	300
CTTCTCCTCT	TGACAGCGAG	GACAGGAGGG	GGACAAGGGG	ACACCTGGGC	AGACCCGCCG	360
GTCTCCCCC	CACCCACCC	CGGCACCTC	GAG			393

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 421 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCGGCC	AAAGAGGCCT	ACGAAGTTAC	AGAAGTGA	TTCTCGGGTC	CCAGACACGC	60
ACCTATGTAC	CTCCCACTGG	TGTCCCTGCA	AAGCCTGGCG	CTTTTGACAT	CAATAATAAA	120
AGTGGCAGGG	CTGAGCAACA	CCTCAGGAGT	TACTCTGGAA	GGATGGAGGA	GTTATGTAAC	180
ACACGAGAGT	CAGGAGCCCT	GTGGAAGTGC	TTTTATTAGC	AGTAAGGCTG	ATCGTACAAA	240
AAATCTCAG	AGCTTCATAG	GACAAGGTAG	TACAAGTATG	GATGATACAG	GACTGAGGAA	300
CGGGGGACGG	CTCAAAAGAA	ATCAACATCG	TCTGGGGCAT	CCAGGTCCCG	ATATTCCACA	360
ATGGCCCTTG	GGTCTCCACG	AACCATCCTG	TGAGGTGAGA	GGTACAGGAT	CAGACCTCGA	420
G						421

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

```

TAGGAGATCT GGATGGCATC TACTTCGTAT GACTATTGCA GAGTGCCCAT GGAAGACGGG      60
GATAAGCGCT GTAAGCTTCT GCTGGGGATA GGAATTCTGG TGCTCCTGAT CATCGTGATT      120
CTGGGGGTGC CTTTGATTAT CTTCAACATC AAGGCCAACA GCGAGGCCTG CCGGGACGGC      180
CTTCGGGGAG TGATGGAGTG TCGCAATGTC ACCCATCTCC TGCAACAAGA GCTGACCGAG      240
GCCCAGAAGG GCTTTCAGGA TGTGGAGGCC CAGGCCGCCA CCTGCAACCA CACTGTGATG      300
GCCCTAATGG CTTCCTTGG ATGCAGAGAA GGCCCAAGGA CAAAAGAAAG TGAAGNATC      360
TCGAG
365

```

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

```

GAATTCGGCC AAAGAGGCCT AACACAGGAA ACATTACAAT TGAACAATGC CTCAGCTATA      60
CATTACATC AGATTATTGG GAGCCTATTT GTTCATCATT TCTCGTGTTC AAGGACAGAA      120
TCTGGATAGT ATGCTTCATG GCACTGGGAT GAAATCAGAC TCCGACCAGA AAAAGTCAGA      180
AAATGGAGTA ACCTTAGCAC CAGAGGATAC CTTGCCTTTT TTAAGTGCT ATTGCTCAGG      240
GCACTGTCCA GATGATGCTA TTAATAACAC ATGCATAACT AATGGACATT GCTTTGCCAT      300
CATAGAAGAA GATGACCAGG GAGAAACCAAC ATTAGCTTCA GGGTGTATGA AATATGAAGG      360
ATCTGATTTT CAGTGCAAAG ATTCTCCAAA AGCCAGCTA CGCCGACAA TAGAATGTTG      420
TCGGACCAAT TTATGTAACC AGTATTGCA ACCCAGCTC GAG
463

```

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

```

GAATTCGGCC AAAGAGGCCT ACTTAGCTTC AAATCCCTAC TCCTTCACTT ACTAATTTTG      60
TGATTGGAA ATATCCGCGC AAGATGTGTA CGTTCAGAC TTGGCTAGTG CAAGCCTTGT      120
TTATTTTCT CACCACTGAA TCTACAGGTG AACTTCTAGA TCCATGTGGT TATATCAGTC      180
CTGAATCTCC AGTTGTACAA CTTCACTTCTA ATTCACTGC AGTTTGTGTG CTAAAGGAAA      240
AATGTATGGA TTATTTTCAT GTAAATGCTA ATTACATTGT CTGGAAAACA AACCATTTTA      300
CTATTCCTAA GGAGCAATAT ACTATCATAA ACAGAACAGC ATCCACGCTC GAG
353

```

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

```

GAATTCGGCC AAAGAGGCCT ACACTCGTCT CTTTTTTTCC CCATCTCATT GCTCCAAGAA      60
TTTTTTTCTT CTTACTCGCC AAAGTCAGGG TTCCCTCTGC CCGTCCCGTA TTAATATTTT      120
CACTTTTGA GA ACTACTGGCC TTTTCTTTT AAAGGAATTC AAGCAGGATA CGTTTTTCTG      180
TTGGGCATTG ACTAGATTGT TTGCAAAAGT TTCGCATCAA AAACAACAAC AACAAAAAAC      240
CAACAACCTC TCCTTGATCT ATACTTTGAG AATTGTTGAT TTCTTTTTTT TATTCTGACT      300
TTTAAAAACA ACTTTTTTTT CCACTTTTTT AAAAAATGCA CTACTGTGTG CTGAGCGCTT      360
TTCTGATCCT GCATCTGGTC ACGGTCGCGC TCAGCCTGTC TACCTGCAAC ACACTCGAG      419

```

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

```

GAATTCGGCC AAAGAGGCCT ACCCAGAAAC ATCCAATTCT CAAACTGAAG CTCGCACTCT      60
CGCCTCCAGC ATGAAAGTCT CTGCCGCCCT TCTGTGCCTG CTGCTCATAG CAGCCACCTT      120
CATTCCCCAA GGGCTCGCTC AGCCAGATGC AATCAATGCC CCAGTCACCT GCTGCTATAA      180
CTTCACCAAT AGGAAGATCT CAGTGCAGAG GTCGCGAGC TATAGAAGAA TCACCAGCAG      240
CAAGTGTCCT AAAGAAGCTG TGATCTTCAA GACCATGTG GCCAAGGAGA TCTGTGCTGA      300
CCCCAAGCAG AAGTGGGTTC AGGATTCCAT GGACCACCTG GACAAGCAAC CCAAACCTCGA      360
G

```

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

```

TAGGACAAAA CAAACATTT TCCCTTGGGG TTTTTTTTTT CTTTCTTTT TCTCCCCTTT      60
ACTCTTTTGG TGGTGTGCT TTTCCTTCC TTTCCTTTT GAGATTTTTT TGTTGTTGTT      120
TCTTTTTTGT ATTTTACTGA TATCACCAGG ATAGTTTACT CTCCTTCTAG CTTTCTGCTT      180
ACCGCACACT GGATAACACA CACATACACA CCCACAAAAA TGCTCATGAA CCAATCCGG      240
AGAAGGTTCC AGCAGGTCCC CCACCCTCCC CTCCTCCTCC TACTTCTCCT CTTGACAGCG      300
AGGACAGGAG GGGGACAAGG GGACACCTGG GCAGACCCGC CGGCTCTCCC CCCACCCAC      360
CCCGGCAC

```

(2) INFORMATION FOR SEQ ID NO:175:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 382 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

```
GAATTCGGCC AAAGAGGCCT AGACTAACCC AGAAACATCC AATTCTCAA CTGAAGCTCG      60
CACTCTCGCC TCCAGCATGA AAGTCTCTGC CGCCCTTCTG TGCCTGCTGC TCATAGCAGC      120
CACCTTCATT CCCCAAGGGC TCGCTCAGCC AGATGCAATC AATGCCCCAG TCACCTGCTG      180
CTATAACTTC ACCAATAGGA AGATCTCAGT GCAGAGGCTC GCGAGCTATA GAAGAATCAC      240
CAGCAGCAAG TGTCCCAAAG AAGCTGTGAT CTTCAAGACC ATTGTGGCCA AGGAGATCTG      300
TGCTGACCCC AAGCAGAAGT GGGTTCAGGA TTCCATGGAC CACCTGGACA AGCAAACCCA      360
AACTCCGAAG ACTTCACTCG AG
```

(2) INFORMATION FOR SEQ ID NO:176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

```
GAATTCGGCC AAAGAGGCCT AGTATAATAC TAAGTTGAGA TGATATCATT TACGGGGGAA      60
GGCGCTTTGT GAAGTAGGCC TTATTTCTCT TGTCCTTTCG TACAGGGAGG AATTGAAGT      120
AGATAGAAAC CGACCTGGAT TACTCCGGTC TGAAGTCAGA TCACGTAGGA CTTTAATCGT      180
TGAACAAACG AACCTTTAAT AGCGGCTGCA CCATCGGGAT GTCCTGATCC AACATCGAGG      240
TCGTAAACCC TATTGTTGAT ATGGACTCTA GAATAGGATT GCGCTGTTAT CCCTAGGGTA      300
ACTTGTCCG TTGGTCAAGT TATTGGATCA ATTGAGTATA GTAGTTCGCT TTGACTGGTG      360
AAGTCTTAGC ATGTACTGCT CGGAGGTTGG GTTCTGCTCC GAGGTCGCCC CAACCGAAAT      420
TTTTAATGCA GGTTCGTTAG TTTAGGACCT GTGGGTTTGT TAGGTACTGT TTGCATTAAT      480
AAATTAAAGC CTCGAG
```

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

```
TTNGGCCAAA GGGGCTTAGG ACAAACAAA ACATTTTCCT TTGGGTTTNA NTTTCTNTCT      60
TTNTTCTCCC ATTTANTNNT GGGGTGGTGT TGCTTTTCCT TTCCTTTTCC CTGGAGATT      120
TTNTNGTTGT NGTTTCCTTT TTGTATTNTA NTGATATCAC CAGGATAGTT TACTCTCNTT      180
NTAGCTNTGT GCTTACCGCA CANTGGATAA CACACACATA CACACCCACA AAAATGNTCA      240
TGAACCCAAT CCGGAGAAGG TTCCAGCAGG TCCCCCACC TCCCCTCCTC CTCNTACTTC      300
TCCTCTNGAC AGCGAGGACA GGAGGGGGAC AAGGGGACAC CTGGGCAGAC CCGCCGGCTN      360
TTCCCCCACC CCCACCCGG CACCCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

```

GAATTCGGCC AAAGAGCAAT TCTCAAAC TG AAGCTCGCAC TCTCGCCTCC AGCATGAAAG      60
TCTCTGCCGC CCTTCTGTGC CTGCTGCTCA TAGCAGCCAC CTTCAATCCC CAAGGGCTCG      120
CTCAGCCAGA TGCAATCAAT GCCCCAGTCA CCTGCTGCTA TAACTTCACC AATAGGAAGA      180
TCTCAGTGCA GAGGCTCGCG AGCTATAGAA GAATCACCAG CAGCAAGTGT CCCAAAGAAG      240
CTGTGATCTT CAAGACCATT GTGGCCAAGG AGATCTGTGC TGACCCCAAG CAGAAAGTGGG      300
TTCAGGATTC CATGGACCAC CTGGACAAGC AAACCCAAAC TCCGAAGACT CTCGAG      356

```

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 480 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

```

GAATTCGGCC AAAGAGGCCT ACCGAGACTG ACACACTGAA CTCCACTTCC TCCTCTTAAA      60
TTTATTTCTA CTTAATAGCC ACTCGTCTCT TTTTTCCTCC ATCTCATTGC TCCAAGAATT      120
TTTTTCTTCT TACTCGCCAA AGTCAGGGTT CCCTCTGCCC GTCCCGTATT AATATTTCCA      180
CTTTTGGAAC TACTGGCCTT TTCTTTTAA AGGAATTCAA GCAGGATACG TTTTCTGTGT      240
GGGCATTGAC TAGATTGTTT GCAAAAGTTT CGCATCAAAA ACAACAACAA CAAAAACCA      300
AACAACTCTC CTTGATCTAT ACTTTGAGAA TTGTTGATTT CTTTTTTTAA TTCTGACTTT      360
TAAAAACAAC TTTTTTTTCC ACTTTTTTAA AAAATGCACT ACTGTGTGCT GAGCGCTTTT      420
CTGATCCTGC ATCTGGTCAC GGTGCGCTC AGCCTGTCTA CCTGCAGCAC CACTCTCGAG      480

```

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 462 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

```

GAATTCGGCC AAAGAGCCTA ACACAGGAAA CATTACAATT GAACAATGCC TCAGCTATAC      60
ATTTACATCA GATTATTGGG AGCCTATTTG TTCATCATTT CTCGTGTTCA AGGACAGAAT      120
CTGGATAGTA TGCTTCATGG CACTGGGATG AAATCAGACT CCGACCAGAA AAAGTCAGAA      180
AATGGAGTAA CCTTAGCACC AGAGGATACC TTGCCTTTT TAAAGTGCTA TTGCTCAGGG      240
CACTGTCCAG ATGATGCTAT TAATAACACA TGCATAACTA ATGGACATTG CTTTGCCATC      300
ATAGAAGAAG ATGACCAGGG AGAAACCACA TTAGCTTCAG GGTGTATGAA ATATGAAGGA      360
TCTGATTTTC AGTGCAAAGA TTCTCCAAAA GCCCAGCTAC GCCGACAAT AGAATGTTGT      420

```

CGGACCAATT TATGTAACCA GTATTGCAA CCCACGCTCG AG

462

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GAATTCGGCC AAAGAGGCCT AACACAGGAA ACATTACAAT TGAACAATGC CTCAGCTATA	60
CATTACATC AGATTATTGG GAGCCTATTT GTTCATCATI TCTCGTGTTT AAGGACAGAA	120
TCTGGATAGT ATGCTTCATG GCACTGGGAT GAAATCAGAC TCCGACCAGA AAAAGTCAGA	180
AAATGGAGTA ACCTTAGCAC CAGAGGATAC CTTGCCTTTT TTAAAGTGCT ATTGCTCAGG	240
GCACTGTCCA GATGATGCTA TTAATAACAC ATGCATAACT AATGGACATT GCTTTGCCAT	300
CATAGAAGAA GATGACCAGG GAGAAACCAC ATTAGCTTCA GGGTGTATGA AATATGAAGG	360
ATCTGATTTT CAGTGCAAAG ATTCTCCAAA AGCCCAGCTA CGCCGGACAA TAGAATGTTG	420
TCGGACCAAT TTATGTAACC AGTATTGCA ACCCAGCTC GAG	463

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

TACGAGAAGT CCTGTAAGAC GTAAATATTT TTAAATTTCA CTGAATTTTT GTCTTTCTCG	60
GTACCATAGA ACACCACAGC CAAGAGATCT CGATCACTGC TTATGATCTT ACTGATGTAC	120
ACACTTTGGA TACACTGGAT GCTCATGTCA AAAGGTGTCA ACTCATCTTC ATCTCCATCC	180
TCTTCCTCAC CATCACCTTC TTCTTCTCCT TCCTCTTCCT CCCCACCTTC TTCCTCTTCT	240
TCGTCTACCT CATTGTGAGC CTCCTGCTCC CCATTTTCCT CATTAGCATT CCCGTTAGCA	300
GGGGCGTCTC TTCCATTTTC TGCCTCTTCC ACAACTTCCT TCTTCTCCTT TAAGTCCTTG	360
GTGGTGAGT	369

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCGGCC NAAGANGCCT ATGATCNTCT TCTTTGAAGA AACATGAAGT TACACTATGT	60
TGCTGTGCTT ACTCTANCCA TCCTGATGTT CCTGACATGG CTTCCACAAT CACTGAGCTG	120
TNACAAAGCA CTCTGTGCTA NTGATGTGAG CAAATGCCTC ATTCAGGAGC TCTGCCNGTG	180
CCGGCCGGGA GAAGCAATTG CTCCTGCTGT NAGGAGTGCA TGCTGTGTCT TGGGGCCCTT	240

TGGGACGANT GCTGTGACTG TGTGGTATG TGTAATCCTC GAAATTATAG TGACACACCG 300
CACCTCNAG 309

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCGGCC AAAGAGGCCT AATTCTGGTT TAAGATTCTA TCCATTTCTC ACTCTCAGAT 60
CTGTTTGTTC CACCCTCTCC CCCTAAATAT TTGGATTTTA TATAGACCAG TAGGCTAAGG 120
TAGGGAAGAC CACTGACAAG TATAAATTTA AGAGTTTACA AAACCAAGGA GGCCATCCAG 180
CCCCTAGTTC TAAGCCATGT TCAGCACAGT GCCAACTTTG CCTTCCCTGG CTGTCCTTGC 240
TTGCTTTCTG GTTGCTGTAA TTCTGAGGGG CAACCAGGCT TGCTGTAGAG AGGAGAGCCA 300
GATGATGTGG AAGCCTAAGG CCACACCCCT CGAG 334

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

TAACCAGCCT TGAAGAGCCC TTCCTCTGGC TTGCTAGGAA GCTCATTGGA GACCCTAACT 60
TGGAATTTGT TGCCATGCCT GCTCTCGCCC CACCAGAAGT TGTCATGGAC CCAGCTTTGG 120
CAGCACAGTA TGAGCACGAC TTAGAGGTTG CTCAGACAAC TGCTCTCCCG GATGAGGATG 180
ATGACCTGTG AGAATGAAGC TGGAGCCCAG CGTCAGAAGT CTAGTTTAT AGGCAGCTGT 240
CCTGTGATGT CAGCGGTGCA GCGTGTGTGC CACCTCATTA TTATCTAGCT AAGCGGAACA 300
TGTGCTTCAT CTGTGGGATG CTGAAGGAGA TGAGTGGGCT TCGGAGTGAA TGTGGCAGTT 360
TAAAAAATAA CTTTATTGTT TGGACCTGCA TATTTAGCTG TTTTGAACG CAGTTGATTC 420
CTTGAGTTTC ATATATAAGA CTGCTGCAGT CACATCACAA TATTCAGTGG TGAATCTTGT 480
TTGTTACTGT CATTCCCATT CCTTTTCGTT TAGAATCAGA AT 522

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTCGGCC AAAGAGGCCT AGGACAAAAC AAAACATTTT CCTTTGGGTT TTTTTTTTCT 60
TTCTTTTTTC TCCCCTTAC TCTTTGGGTG GTGTTGCTTT TCCTTTCCTT TTCCCTTTGA 120
GATTTTTTTG TTGTTGTTTC CTTTTGTAT TTTACTGATA TCACCAGGAT AGTTTACTCT 180

CCTTCTAGCT TTCTGCTTAC CGCACACTGG ATAACACACA CATAACACACC CACAAAAATG	240
CTCATGAACC CAATCCGGAG AAGGTTCCAG CAGGTCCTCCCT CCTCCTCCTA	300
CTTCTCCTCT TGACAGCGAG GACAGGAGGG GGACAAGGGG ACACCTGGGC AGACCCGCCG	360
GCTCTCCCCC CACCCACCC CGGCACCTC GAG	393

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTCGGCC AAAGAGGCCT ATTCTAGGAC AAGAGCCAGG AAGAAACCAC CGGAAGGAAC	60
CATCTCACTG TGTGTAAACA TGACTTCCAA GCTGGCCGTG GCTCTCTGG CAGCCTTCCT	120
GATTTCTGCA GCTCTGTGTG AAGGTGCAGT TTTGCCAAGG AGTGCTAAAG AACTTAGATG	180
TCAGTGATA AAGACATACT CCAAACCTTT CCACCCCAA TTTATCAAAG AACTGAGAGT	240
GATTGAGAGT GGACCACACT GCGCCAACAC AGAAATTAT GTAAAGCTTT CTGATGGAAG	300
AGAGCTCTGT CTGGACCCA AGGAAACTG GGTGCAGAGG GAGCTCGAG	349

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GAATTCGGCC AAAGAGGCCT ACAAGAAAGC AAGCTCATCA TACTGGCTAG TGGTGGACCC	60
CAAGCTTTAG TAAATATAAT GAGGACCTAT ACTTACGAAA AACTACTGTG GACCACAAGC	120
AGAGTGCTGA AGGTGCTATC TGTCTGCTCT AGTAATAAGC CGGCTATTGT AGAAGCTGGT	180
GGAATGCAAG CTTTAGGACT TCACCTGACA GATCCAAGTC AACGTCTGT TCAGAACTGT	240
CTTTGGACTC TCAGGAATCT TTCAGATGCT GCAACTAAAC AGGAAGGGAT GGAAGGTCTC	300
CTTGGGACTC TTGTTGAGCT TCTGGGTTCA GATGATATAA ATGTGGTCAC CTGTGCAGAT	360
CTCGAG	366

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TACAGCCACA TCTGGATACA CACACACACT CTTACATTCA TACCCAGAGA CTGGTGACACA	60
GACACACACA CATCCCCCGT CCTGCCAATC AGTCCCAGGA ACACACAGGT CTCTATCAAC	120
ACCCAGAAAT TCTGACACCA CAAGCACAGG CCAACCTACA GCTAGAGGAT TAATGTCCAG	180

ACCCACAGGC TGGTGTGCGC ATGTCCTTCC ACGTGAATGT CACATGGGAG GACAGACTGC	240
ATGGATT TTTT TTAATGACAC TATTTTATTT ATTTTGTGAG ACAGAGTCTC ACTCTGTCCG	300
CCAGGATGGA GTGCAGTGGC GTGATCTCGG CTCACTACAA CCTCCGCCTC CTGGGTTCAA	360
GCGATTCTCG TGCCTCAGCA TCCCAAGTAC CTGGGATTAC AGGCGCATGC CACCACGTCC	420
A	421

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GAATTCGGCC AAAGAGGCCT AGGGAGATCT GGATGGCATC TACTTCGTAT GACTATTGCA	60
GAGTGCCCAT GGAAGACGGG GATAAGCGCT GTAAGCTTCT GCTGGGGATA GGAATTCTGG	120
TGCTCCTGAT CATCGTGATT CTGGGGGTGC CCTTGATTAT CTTCAACATC AAGGCCAACA	180
GCGAGGCCTG CCGGGACGGC CTTGGGCGAG TGATGGAGTG TCGCAATGTC ACCCATCTCC	240
TGCAACAAGA GCTGACCGAG GCCCAGAAGG GCTTTCAGGA TGTGGAGGCC CAGGCCGCCA	300
CCTGCAACCA CACTGTGATG GCCCTAATGG CTTCCCTGGA TGCAGAGAAG GCCCAAGGAC	360
AAAAGAAAAA GGAGGAGCTC GAG	383

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAATTCGGCC AAAGAGGCCT ACCCCAGTCC AGATCCAGGA CTGAGATCCC AGAACCATGA	60
ACCTGGCCAT CAGCATCGCT CTCCTGCTAA CAGTCTTGCA GGTCTCCCGA GGGCAGAAGG	120
TGACCAGCCT AACGGCCTGC CTAGTGGACC AGAGCCTTCG TCTGGACTGC CGCCATGAGA	180
ATACCAGCAG TTCACCCATC CAGTACGAGT TCAGCCTGAC CCGTGAGACA AAGAAGCACG	240
TGCTCTTTGG CACTGTGGGG GTGCCTGAGC ACACATACCG CTCCCGAACC AACTTCACCA	300
GCAAATACAA CATGAAGGTC CTCTACTTAT CCGCCTTCAC TAGCAAGGAC GAGGGCACCT	360
ACACGTGTGC ACTCCACCAC TCTGGCCATT CCCCACCAT CTCCTCCCAG AACGTCACCA	420
GTCTCGAG	428

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAATTCGGCC AAAGAGGCCT AAAGAGCTCT CACTTCAGTC TTACTTACCC CACTGCTATT	60
CCCTGTGGAG AAAGCCGGCT AATTGTTTTG ATAAGGCTAT CTGCCATTGT AGAATACCTT	120
TCTCTAGTAG CTGAATGACA ATCAACTATA CGTTCCATAC TAAACATGCC AGAGATAGGA	180
CTTTTAGGCC TTGCTTTACA AAAGTGGTTT TTAACAGCTG ACATGAATAT TTCCCGTTTC	240
TATTTCTTT TTTTTTTTT TTTTTTTTT TGAGACGGAG TCTCGCTCTA TCCCCACGC	300
TCGAG	305

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 0 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 516 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAATTCGGCC AAAGAGGCCT AANAGAAGAT GCCCCTGCTG ATCACTCTAA CCTGCTCCTC	60
TTCTGGCTCT CAGGCTACTC CATTGCCACT CAAATCACCG GTCCAACAAC AGTGAATGGC	120
TTGGAGCGGG GCTCCTTGAC CGTGCACTGT GTTACAGAT CAGGCTGGGA GACCTACTTG	180
AAGTGGTGGT GTCGAGGAGC TATTTGGCGT GACTGCAAGA TCCTTGTTAA AACCAGTGGG	240
TCAGAGCAGG AGGTGAAGAG GGACCGGGTG TCCATCAAGG ACAATCAGAA AAACCGCACG	300
TTCATGTGA CCATGGAGGA TCTCATGAAA ACTGATGCTG ACACTTACTG GTGTGGAATT	360
GAGAAAACCTG GAAATGACCT TGGGGTCACA GTTCAAGTGA CCATTGACCC AGCACCAGTC	420
ACCCAAGAAG AAACAGCAG CTCCCAACT CTGACCGGCC ACCACTTGGA CAACAGGCAC	480
AAGCTCCTGA AGCTCAGTGT CCTCCACCC CTCGAG	516

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 466 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GAATTCGGCC AAAGAGGCCT AGCGCCCTGA AGACAGAATG TTCCATATCA GAGCTGTGAT	60
CTTGAGAGCC CTCTCCTTGG CTTTCCTGCT GAGTCTCCGA GGAGCTGGGG CCATCAAGGC	120
GGACCATGTG TCAACTTATG CCGCGTTTGT ACAGACGCAT AGACCAACAG GGGAGTTTAT	180
GTTTGAATTT GATGAAGATG AGATGTTCTA TGTGGATCTG GACAAGAAGG AGACCGTCTG	240
GCATCTGGAG GAGTTTGGCC AAGCCTTTTC CTTTGAGGCT CAGGGCGGGC TGGCTAACAT	300

TGCTATATTG AACAACTACT TGAATACCTT GATCCAGCGT TCCAACCACA CTCAGGCCAC	360
CAACGATCCC CCTGAGGTGA CCGTGTTCCT CAAGGAGCCT GTGGAGCTGG GCCAGCCCAA	420
CACCCTCATC TGCCACATTG ACAAGTTCTT CCTACCACTG CTCGAG	466

(2) INFORMATION FOR SEQ ID NO:196:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 191 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

TAGGCAGAAT GGGACTCCAA GCCTGCCTCC TAGGGCTCTT TGCCCTCATC CTCTCTGGCA	60
AATGCAGTTA CAGCCCGGAG CCCGACCAGC GGAGGACGCT GCGCCAGGC TGGGTGTCCC	120
TGGGCCGTGC GGACCCTGAG GAAGAGCTGA GTCTCACCTT TGCCCTGAGA CAGCAGAATG	180
TGGATCGACG T	191

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 614 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTCGGCC AAAGAGGCCT AATGGATCTC ATGTGCAAGA AAATGAAGCA CTGTGGTTCT	60
TCCTCCTGCT GGTGGCGGCT CCCAGATGGG TCCTGTCCCA GCTGCAGCTG CAGGAGTCGG	120
GCCCAGGACT GGTGAAGCCT TCGGAGACCC TGTCCTCAC CTGCACTGTC TCTGGTGGCT	180
CCATCAGCAG TAGTAGTTAC TACTGGGGCT GGATCCGCCA GCGCCAGGG AAGGGGCTGG	240
AGTGGATTGG GAGTATCTAT TATAGTGGGA GCACCTACTA CAACCCGTCC CTAAGAGTC	300
GAGTCACCAT ATCCGTAGAC ACGTCCAAGA ACCAGTTCTC CCTGAAGCTG AGCTCTGTGA	360
CCGCCGCAGA CACGGCTGTG TATTACTGTG CGAGACATTC TGGGCGCAGC AGCTGGTTCA	420
CGTCCTACTG GGGCCAGGGA ACCCTGGTCA CCGTCTCCTC AGGGAGTGCA TCCGCCCAA	480
CCCTTTTCCC CCTCGTCTCN TGTGAGAATT CCCCGTCGGA TACGAGCAGC GTGGCCGTTG	540
GCTGCCTCGC ACAGGACTTC CTTCCCGACT CCATCACITT CTCCTGGAAA TACAAGAACA	600
ACTCTGAACG CGAG	614

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 0 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 427 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

```
GAATTCGGCC AAAGAGGCCT ANACTGCAGC TCTTTTCATT TTGCCATCCT TTTCCAGCTC      60
CATGATGGTT CTGCAGGTTT CTGCGGCCCC CCGGACAGTG GCTCTGACGG CGTTACTGAT      120
GGTGCTGCTC ACATCTGTGG TCCAGGGCAG GGCCACTCCA GAGAATTACC TTTTCCAGGG      180
ACGGCAGGAA TGCTACGCGT TTAATGGGAC ACAGCGCTTC CTGGAGAGAT ACATCTACAA      240
CCGGGAGGAG TTCGCGCGCT TCGACAGCGA CGTGGGGGAG TTCCGGGCGG TGACGGAGCT      300
GGGGCGGCCT GCTGCGGAGT ACTGGAACAG CCAGAAGGAC ATCCTGGAGG AGAAGCGGGC      360
AGTGCCGGAC AGGATGAGCA GACACAATA CGAGCTGGGC GGGCCCATGA CCCTCACAGA      420
ACTCGAG                                         427
```

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

```
TAGGGATGTC AACATGATCT TTTCATATAT GCTGGCTATA GAAATTGGTC TCGGTGAAGT      60
AATGGTCTGT CTGTCAAGCA TGACATCCTT GCCTGTGTTA AGTTTTGTGT GCTCTTCTGG      120
GATGTTGATC GTGACGTCTT TTCCGGGATT GAGAAGCTTC TGTTGCTCTT CTGGGATGTC      180
ATTCATGATC TCTTCATATA TGCTGGCTAT AGAAATTGGG CTCTGTGAAG AAATAGTGTG      240
TCCCAACCT TGGTACAGNC CCCCTGGGGA GGGTACCTTT GAAGAACCAG AAGTTAGANC      300
TTGTGAAGAA GAAGAAAGTA GG                                         322
```

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 272 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```
GAATTCGGCC AAAGAGGCCT ATGGAGTGTG AGAACAGCAA AAAATAATAA TTCAACCAGT      60
TGGTTATTAT GAACATCATT TTCTATTTTT TAAAAATATG CTATATCATG GAATTCAATG      120
TAAACCTCA AGAGATGCCA TCCTTGGAGA GGGCTGCACC AGCCTGTGCC CCAAGTTACC      180
CAGGATCACC CCCTACTTCT CCTGACGGCC CCCCAGAGAA GGCCTGCATT CTGGGCGACG      240
TGGCCTTCAG GGGCTCAACC CTTGGCCTCG AG                                         272
```

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```
GAATTCGGCC AAAGAGGCCT AGCCAATTTG GTTTTCTAAG TATTTTCACG CCTTCTCCTC      60
GTGTCCGCGT CACTGCTCTG ATTCAGGCCC TTGTCATTTT TCATCTTTGC CATTTTAGTA      120
GTTTTTGGAT TGGGCTCCCG GCTGCTAATT TTGTCCTTTC TTCCACTATC TTCCACATTG      180
TCACCGCAGT CATGTTTCTA AGGCAGAATC TCACTGTGCC CCACATCGTG TTGCTGGGCC      240
CTTGCAATGCC GTACCCCTGGC CTTTGTGAAA TGCCCTTCAT CTGTGCTCTT CCCTCCACCT      300
GGAATGTCCG TCTCTCTTTT TCTGCCAACC CACNCGACCC CTCCTCTCTN CAAGCCCGTG      360
AGTGTCCCN CCCTCCATGT CCTGTGGTGA CAGAGCTCGA G                               401
```

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

```
GAATTCGGCC AAAGAGGCCT ACGATATTTG CTGCGACCCG CAGGCGCTAT CCGCTGCCGG      60
GTTCTGGCGC GCCCTTTCAG TTCTGCTTGC TGTCGCACC GNTGCGTTAC CCGGAACCGC      120
CGGGCCGAAC AGCATGACGT CCGCTTTGGA GAACTACATC AACCGAACGT TTGCCGTTAT      180
TACATCAGAT GGGAGAATGA TTGTGGGAAC ACTGAAAGGT TTTGACCAGA CCATTAATTT      240
GATTTTGGAT GAAAGCCATG AACGAGTATT CAGCTCTTCA CAGGGGGTAG AACAAGTGGT      300
ACTAGGATTA TACATTGTAA GAGGTGACAA CGTTGCAGTC ATTGGAGAAA TCGATGAAGA      360
AACAGATTCT GCGCTTGATT AGGGGAACAC TCGAG                               395
```

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

```
GAATTCGGCC ANAGAGGCCT AAGAGCCAGT AAAAAAATTG TTAGAAAGCA GATACCATCA      60
AATTGGTTCT GGGAAAGTGT AAATCAAAGT TGCACAACCC AAAGAGGTAT ATAGGCAGCA      120
ACAGCAACAA CAAAAAGGTG GAAGAGGTGC TGCAGCTGGT GGACGAGGTG GTACGAGGGG      180
TCGTGGCCGA GGTCAAGGCC AAAACTGGAA CCAAGGATTT AATAACTATT ATGATCAAGG      240
ATATGGAAAT TACAATAGTG CCTATGGTGG TGATCAAAAC TATAGTGGCT ATGGCGGATA      300
TGATTATACT GGTATAACT ATGGGAAC TAAGATATGGA CAGGGATATG CAGACTACAG      360
TGGCCAACAG AGCACTTATG GCAAGGCATC TCGAG                               395
```

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

```
GAATTCGGCC AAAGAGGCCT AGTTTGGTCG TTCGTTGGGC GGTGCTGGTT TTTCGCTCGT    60
CGACTGCGGC TCTTCCTCGG GCAGCGGAAG CGGCGCGGCG GTCGGAGAAG TGGCCTAAAA    120
TTTCGGCGTT GGGTGAAGA AAATGGCCCG AACCAAGCAG ACTGCTCGTA AGTCCACCGG    180
TGGGAAAGCC CCCCGCCAAA CAGTTGNCCA CGGAAANCCG CCAGGAAAAG CGCTCCNTCT    240
ACCGGCGGGG TGAAGAAGCC TCATCGCTAC AGGCCCGGGA CCGTGGCGCT TCGAGAGATT    300
CGTCGTTATC AGAAGTCGAC CGAGCTGCTC ATCCGGAAGC TGCCCTTCCA GAGGTTGGTG    360
AGGGAGATCG CGCAGGATT CAAAACCGAC CTGAGGTTTC AGAGCGCAGC CATCGGTGCG    420
CTGCAGGAGG CTAGCGAAGC GTACCTGGTG GGTCTGTTTC AAGATACCAA CCTGTGTGCC    480
ATCCACGCTA AGAGAGTCAC CATCATGCCC AAAGACATCC AGTTGGCTCG CCGGATACGG    540
GGAGAGAGAG CTTTCTCGAG
```

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

```
GAATTCGGCC AAAGAGGCCT ACTAGTTTAC TTTATCCCAT CCATTTATAT ATACATATAT    60
ATACACATAT ATGTGTGTTG TTTTGTGTTT GTTTGTGTTT GTTTTGTGA GATGGAGTCT    120
CGCTCTGTCT CCCAGGCTGG AGTGCAGTGG TGTGATCTTG GCTCACTGCA ACCTCTGCCT    180
CCTGGGTTC AAGCAATTCTC CTGCCTCAGC TTCCCGAGT AGCTGGGACT ACAGGTGTGC    240
GCCACCACGC CCGGCAAATT TTTTTTTTTT TTTTTTTTTT TTGATATTTT TAGCAGAGAT    300
GAGGTTTCCC CACGTTGGCC AGGCTGGTCT CGAACTCTTG ACCTCAGGTT ATCTGCCTGC    360
CTTGGCCTCC CAAAGTGTG GGATTACAGG CGTGAGCCAC CGAACCTCGA G    411
```

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 0 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GAATTCGGCC AAAGAGGCCT ACGTGGTGCG CGAGAGCGTA TCCCCAACTG GGA	60
GGCAACTTGA ACTCAGAACA CTACAGCGGA GACGCCACCC GGTGCTTGAG GCGG	120
GGCGCACAGA GACCGAGGCG CATAGAGACC GAGGCACAGC CCAGCTGGGG CTAG	180
TGGGAAAGGA GAGCGTCGTT AATTATTTC TTATTGCTCC TAATTAATAT TTATAT	240
TTATGTACGT CCTCCTAGGT GATGGAGATG TGTACGTAAT ATTTATTTTA ACTTATG	300
GGGTGTGAGA TGTCCCNCCT GCTGTAAATG CAGGTCTCTT GGTATTTAT GAGCTT	360
GGACTGGTGG AAGCAGGACA CCTGGAACCTG CGCCAAAGTA GGCGACTCGA G	411

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GAATGCTGAT TGACCAGCTA AAAATCAAAT TACAAGATAG CCAAATAAC TTACAGATTA	60
ATGTATCTGA ACTTCAGACA TTGCAGTCTG AACATGNTAC ACTGCTAGAA AGGCACAACA	120
AGATGCTGCA GGAAACTGTG TCTCAGCTCG AG	152

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GAATTCGGCC AAAGAGGCCT ACACNTCTGC ACCTCAACCA CAGACTACAC TTGCTGA	60
GGCTCCTGGG GCCATGAGGC TGTCACTGCC ACTGCTGCTG CTGCTGCTGG GAGCCTGGG	120
CATCCAGGG GGCCTCGGG ACAGGGCGCC ACTCACAGCC ACAGCCCCAC AACTGGATGA	180
TGAGGAGATG TACTCAGCCC ACATGCCCGC TCACCTGCGC TGTGATGCCT GCAGAGCTGT	240
GGCTTACCAG GTGAGTCCTT CACCACTGTC ACCCTGCCCT GCTCACACCC CTTCTCAAGC	300
CAGACCCCTC CACCCACCTC ACATTCCACC ACCGGCCTTT GATCCCCGCC TCGAG	355

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 403 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GAATTCGGCC	AAAGAGGCCT	AATTATAAGC	ACTCAATAAT	ACATTATCAA	CTATTATTAC	60
TCAATTAAAA	CTGGTTAACT	TTAATTGAAT	TTGAACTGCC	ACCTAGAATA	GACAAGAAAA	120
TGAAACACAA	TTCTGTATGG	ATGTCAGAAA	CATGAAATAT	AAAATGTAAT	AAATAAAAAAT	180
ATTAAAAACC	CCTTAGCAAA	TGTTAAGGAG	CGTGTCAAAAT	GATTCCTGTG	TTGAACCTTA	240
AGCATTTAGG	TGGCTGGAGC	CTTGAAAGTT	ACCATCCCCC	AATTTTCTGC	TGTGTCACTA	300
GGTTTTTTTC	TATTGAGCAA	TTCTTTCAGG	TGCGCTCCAC	TCTGCTCTGC	CTAAAGGACA	360
ACTTCATATA	GTGCATTTCGT	GTCTTAGACT	CCACGATCTC	GAG		403

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GAATTCGGCC	AAAGAGGCCT	AAGCGCTAAG	CCTGGAGTGT	GGGCACTGCA	GTTTCAGAGG	60
CACCGATTAT	GAGAATGTGC	AGCTCCACAT	GGGCTCCATT	CATCCTGAGT	TCTGTGATGA	120
TATGGATGCC	GGGGGCCTGG	GCAAGCTCAT	CTTTTACCAG	AAGAGTGCAA	AGCTCTTCCA	180
TTGCCATAAG	TGCTTCTTCA	CCAGCAAGCT	GTACGCCAAT	GTGTACTATC	ACATCACGGC	240
CAGACACGCA	GCCTCGGACA	AGTGGAGTGA	GCAGCCGAAA	GAGCAGCCGA	GCAAAGACAC	300
CCGTCGAG						308

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GAATTCGGCC	AAAGAGGCCT	ACTGTGGTAA	TTCTAGAGCT	AATACATGCC	GACGGGCGCT	60
GACCCCTTTC	GCGGGGGGGA	TGCGTGCAAT	TATCAGATCA	AAACCAACCC	GGTCAGCCCC	120
TCTCCGGCCC	CGGCCCGGGG	GCGGGCGCCG	GCGGCTTTGG	TGACTCTAGA	TAACCTCGGG	180
CCGATCGCAC	GCCCCCGGTG	GCGGCGACGA	CCCATTCGAA	CGTCTGCCCT	ATCAACTTTC	240
GATGGTAGTC	GCCGTGCCTA	CCATGGTGAC	CACGGGTGAC	GGGGAATCAG	GGTTCGATTC	300
CGGAGAGGGA	GCCTGAGAAA	CGGTTACCAC	ATCCAAGGAA	GGCAGCAGGC	GCGCACCTCG	360
AG						362

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GAATTCGGCC	AAAGAGGCCT	ATTCTTTTTT	AAACTAATCA	CCATATTGTA	AATTCAGGG	60
TTTTTTTTTT	GGTTTAAGCT	GACTCTTNGC	TCTAATTTTG	GAACAAAAAGA	AATGTGAAGG	120
GTCAACTCCA	ACGTATGTGG	TTATCTGTGA	AAGTTGCACA	GCGTGGCTTT	TCCTAAACTG	180
GTGTTTTTCC	CCCGCATTTG	GTGGATTTT	TATTATTATT	CAAAAACATA	ACTGAGTTTT	240
TTAAAGAGG	AGAAAATTTA	TATCTGGGTT	AAGTGTTTAT	CATATATATG	GGTACTTTGT	300
AATATCTAAA	AACTTAGAAA	CGGAAATGGA	ATCCTGCTCA	CAAAATCACT	TTAAGATCTT	360
TTCGAAGCTG	TTAATTTTTC	CTAGTGTGTG	GGACACTGCA	GACTTGTCCA	GTGCTCCAC	420
GGCCTGTACG	GACACGACTC	TCGAG				445

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GAATTCGGCC	AAAGAGGCCT	ACTTCACTCT	CTCATTCTTA	GCTTGAATTT	GGAAATGACT	60
TTTGATGACC	TAAAGATCCA	GACTGTGAAG	GACCAGCCTG	ATGAGAAGTC	AAATGGAAAA	120
AAAGCTAAAG	GTCTTCAGTT	TCTTTACTCT	CCATGGTGGT	GCCTGGCTGC	TGCGACTCTA	180
GGGGTCTTTT	GCCTGGGATT	AGTAGTGACC	ATTATGGTGC	TGGGCATGCA	ATTATCCCAG	240
GTGTCGTACC	TCCTAACACA	AGAGCAAGCA	AACCTAACTC	ACCAGAAAAA	GAAACTGGAG	300
GGACAGATCT	CAGCCCGGCA	ACAAGCAGNA	GAAGCTGTTT	TCGAG		345

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTCGGCC	AAAGAGGCCT	ACTGGGGAGT	CTGCTATATT	GTTGTTAAGG	TCTCTTTGTT	60
AGTGGTGGTA	GAAATTGGAG	TATTCCCTCT	CATTGTGGT	TGGTGGCTGG	ATATCTGTTT	120
CTTGAAATG	TTTGATGCTA	CTCTGAAAGA	TCGAGAACTG	AGCTTTCAGT	CGGCTCCAGG	180
TACTACCATG	TTTCTGCATT	GGCTAGTGGG	AATGGTATAT	GTCTTCTACT	TTGCCTCCTT	240
CATTCTATTA	CTGAGAGAGG	TACTTCGACC	TGGTGTCTCT	TGGTTTCTAA	GGAATTTGAA	300
TGATCCAGAT	TTCAATCCAG	TACAGGAAAT	GATCCATTTG	CCAATATATA	GGCATCTCCG	360
AAGATTTATT	TTGTCACTGA	TTGTCTTTGG	CTCCATTGTC	CTCCTGATGC	TTTGGCTTCC	420
TATACGTATA	ATTAAGAGTG	TGCTGCCTAA	TTTTCTTCCA	TACAATGTCA	TGCTCTACAG	480
TGATGCTCCA	GTGAGTGAAC	TGTCCCTCGA	G			511

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GAATTCGGCC AAAGAGGCCT AGTTTATACC CACAGAATTT TTTCATAAAA TTAACCAAAC	60
CCTTTTCACT TTGCTTAAGA CTTCACTTTT GTCCCATTAC TCTTTAAGGT TAAGACCATC	120
TATAAAATCC TCTGAAGTGG ACAAATTTAC ATTCTCTTTA NCAAAATCCA TATTCCTATG	180
CCTTCTTATA ATCTTTTACC AAAAACACCT TCCCTATACA CCTTGTACGT AAAACTGTTT	240
CTCCAGTGGT CTCAACTACA TATTATACTG TTAACCTCTA CTCCTTTTAG CATAGCTAGT	300
AGGCATGGCT CTCCATATGT TCCCAGGCAT CTCGAG	336

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTCGGCC AAAGAGGCCT AGTGGGTAGA TACAGACCCT AACTTTGAGC TCTAAGATGA	60
AAATTTGTTA TAAATCCCTA GTTCCATTC AGTTTTTCA ATATTTATCA AACACCTACT	120
GTGCCAGGCA TTGTTTAGGC ACAGGGGATA CAGCAGAAAA ACTCGAG	167

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GAATTCGGCC AAAGAGGCCT ACACACGCCT TTGGCACAAT GAAGTGGGTA ACCTTTATTT	60
CCCTTCTTTT TCTCTTTAGC TCGGCTTATT CCAGGGGTGT GTTTCGTGCA GATGCACACA	120
AGAGTGAGGT TGCTCATCGG TTAAAGATT TGGGAGAAGA AAATTTCAAA GCCTTGGTGT	180
TGATTGCCTT TGCTCAGTAT CTTCAGCAGT GTCCATTGTA AGATCATGTA AAATTAGTGA	240
ATGAAGTAAC TGAATTTGCA AAAACATGTG TTGCTGATGA GTCAGCTGAA AATTGTGACA	300
AATCACTTCA TACCCTTTT GGAGACAAAT TATGCACAGT TGCAACTCTT CGTGAAACCT	360
ATGGTGAAAC CCTCGAG	377

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

CTTGGGGGTG	GGTTCNNNT	ANNAAAAATT	ANAGNCGTTG	GGGGTTGGGG	GGCNGAGAAG	60
GAANANAGAA	CCCCNGGNAA	AATTTGAAAA	CNGGGTNATT	TATCCNGTNT	TTTNAANGAG	120
AATCCCANNC	CCGGAAAAAA	AAAAAAAANG	AGGAANANAN	AGATTGTAAG	TTAAAACAAA	180
AATCTATCTG	TATAAGTCTT	TACTTGTACA	AGTCTGTACA	AGTCAGTNAG	GTTTGGTCTC	240
TGCAGAGCCA	GAAGGTGATT	TAATTGTAGG	CNTCTTTGGT	AGGCCTCTTT		300
GGCCGAATTC						310

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GAATTCGCCC	AAGAGGCCTA	AAGAGGCCTA	GAAGCCAAAA	AACTTTCCCT	GAAAGGAGTC	60
TTACACAAAG	AGCTCCCATC	TGGCAAGAAA	TACCTCCGCT	ACACACCCCA	GCCTTAAGTC	120
TCTTGAGAA	GCTGGTGCTG	TGAGCCAGAG	GATGTCAGCT	GCCAATTGTG	TTTTCCTGCA	180
GCAATTCAT	AAACACATCC	TGGTGTATC	ACAGCCAAGG	TTTTTAGGTT	GCTATACCAA	240
TGGCTTATTA	AATGAAAATG	GCACTAAAAG	TTCTTGAGA	TTCTTTATAC	TCTCTGCCTT	300
CAGCAATCTC	GAG					313

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GAATTCGGCC	AAAGAGGCCT	AGGAACCACT	GGCTGGTG	ATTTTGCTAG	ATTTTCTGA	60
TTTTTAAACT	CCTGAAAAAT	ATCCAGATA	ACTGTCATGG	AGCTGGTAAC	TATCTTCCTG	120
CTGGTGACCA	TCAGCCTTTG	TAGTACTCT	GCTACTGCCT	TCCTCATCAA	CAAAGTGCCC	180
CTTCCTGTTG	ACAAGTTGGC	ACCTTTACCT	CTGGACAACA	TTCTTCCCTT	TATGGATCCA	240
TTAAAGCTTC	TTCTGAAAC	TCTGGGCATT	TNTGTTGGGC	ACCTTGTGGA	GGGGCTAAGG	300
AAGTGTGTAA	ATGAGCTGGG	ACCAGAGGCT	TCTGAAGCTG	TGGAGCAACC	GCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GAATTCGGCC	AAAGAGGCCT	ATTAAATGTG	TCATTGGAAG	CCATCCCTTT	TTTACATT	60
CATACAACAG	AAACCAGAAA	AGCAATACTG	TTCCATTTT	AAGGATATGA	TTAATATTAT	120

TAATATAATA ATGATGATGA TGATGATGAA AACTAAGGAT TTTTCAAGAG ATCTTTCTTT	180
CCAAAACATT TCTGGACAGT ACCTCGAG	208

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

TNAAACCAAT AGTTTTTTAA AAGACAAGCT TGGGTGGGTG CANGNTGGGG ACAGTGCTGG	60
TCTTTCACNG CAGCCCAGGC ACCNNTTGAG AGTCCCAGNG NNGTGNATGC CCCGAGCCAG	120
TNAAGATGAA GGGAGAGCGG GTGCGGGGGC CATCNTCGGN GTCCCAGCCC GGCCCATGGG	180
ANTGAGTNGC GGCCTCTGCT TGTCGACNTG GGNGCTGGCT GTCCNATTTT ACTACTATTG	240
ACCCCTGAAGG CCATCGAGGA GGGCAGCATG GAGGAGATCG AAGAGGAGGT CCGGCAGAAG	300
AAATCATCAC GGAAGCGCAA GCGAGACTAG GCNTCTNTGG CCGAATTC	348

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GAATTCGGCC AAAGAGGCCT ACTTTCTCTG CAGATCATGG GGGCCTTGAT TGTGCTGTG	60
GGATTGTGTT TCTTCGTGGT TGCCCATGTT AAGAAGAGAA ACACGCTGAA TGCTGGCCAG	120
GATGCCTCTG AGAGAGAAGA GGGACAGATC CAGATTATGG AGCCTGTCCA GGTCACTGTA	180
GGTGACTCGG TAATAATATT TCCACCCCTT CCACCACCTT ACTTTCCTGA ATCTTCAGCT	240
TCTGCGGTCG CTGAGAGTCC TGGAACTAAC AGTCTGCTTC CGAATGAAAA CCCCCCTTCA	300
TATTACAGTA TTTTCAACTA TGGCAGGACC CCAACTTCAG AGGGTGACGC CTCTGAAAGA	360
GATTGTGAAT CTATATATAC CATTCTGGG ACGAATTCAT CTTCTGAGGC CTCACACACT	420
CCACATCTTC CATCTGAATT GCCTCCTAGA TATGAAGAAA AAGAAAATGC TGCAGCACTC	480
GAG	483

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GAATTCGGCC AAAGAGGCCT ACGATTACAA TCATGATTTC CAGAATGGAG AAGATGACGA	60
TGATGATGAA GATATTGATT ATGTTTGCTC TTGGAATGAA CTACTGGTCT TGCTCAGGTT	120
TCCCAGTGTA CGACTACGAT CCATCCTCCT TAAGGGATGC CCTCAGTGCC TCTGTGGTAA	180

AAGTGAATTC CCACTCACTG AGTCCGTATC TGTTCGGGC ATTCAGAAGC TCATTAAAAA	240
GAGTTGAGGT CCTAGATGAG AACAACTTGG TCATGAATTT AGAGTTCAGC ATCCGGGAGA	300
CAACATGCAG GAAGGATTCT GGAGAAGATC CCGCTACATG TGCCTTCCAG AGGGACTACT	360
ATGTGTCCAC AGCTGTTTGC AGAAGCACCG TGAAGGTATC TGCCCAGCAG GTGCAGGGCG	420
TGCATGCTCG CTGCAGCTGG TCCTCCTCCA CGTCTGAGTC TTACAGCAGC GAAGAGATGA	480
TTTTTGGGGA CACTCTCGAG	500

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GAATTCGGCC AAAGAGGCCT AGGAGAAAGA AGATATTGAC ACCATCTACG GGCACCATGG	60
AACTGCTTCA AGTGACCATT CTTTTCTTC TGCCAGTAT TTGCAGCATT AACAGCACAG	120
GTGTTTTAGA GGCAGCTAAT AATTCATTG TTGTTACTAC AACAAAACCA TCTATAACAA	180
CACCAAACAC AGAATCATT CAGAAAAATG TTGTCACACC AACAACTGGA ACAACTCCTA	240
AAGGAACAAT CACCAATGAA TTACTIONAAA TGCTCTGAT GTCAACAGCT ACTTTTTTAA	300
CAAGTAAAGA TGAAGGATTG AAAGCCACAA CCACTGATGT CAGGAAGAAT GACTCCATCA	360
TTTCAAACGT AACAGTAACA AGTGTTACAC TTCCAAATGC TGTTCACAA TTACAAAGTT	420
CCAAACCCAA GACTGAAACT CAGAGTTCAA TTAACAAC AGAAATACCA GGTAGTGTTT	480
TACAACCAGA NCTCGAG	497

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GAATTCGGCC AAAGAGGCCT ACTTTTTTAA TATAAATTTT GTTGATATGG AATTAGGTAA	60
GTTTAAAGTGT CTATGTGCAT ATGTTTTTTA TATAAGTTTT TTCTATTCA TTTACNGAT	120
CCAACTGGCA GTGGTAAAT ATGGCGAGCT CGAG	154

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GAATTCGGCC AAAGAGGCCT AGGAATGGTT TTNATTGGT CCTTATTTTT AACCTGCCCC	60
TGAGACTTAT ATGCTTGTTT ATACCATGTA CGTAGTGTGT GATTGTATGT GTTTGTATTT	120

GTCCACATGT CCCAAAACAT GGGCTGTTAC TCCCTTTTCT ATCTTGTTTT CCTTATTCCC	180
ACCCCTTCTCT TTCCACCCAG GTATCTGGAC AGGAAGACTT CTACCATCAG CTTTACCAGA	240
GGAAGCTGCA GGCCCCACTG TGGCCCAGCT CCTGGGCAT CACTGATTGC TATCAGTATG	300
TCACCTCCTG TCACCCCAAG AGATCAGAGA GACGCAAGTA TGGCCGAGAC TTCCTGCTAC	360
GTTTCCGCTT CTGCAGCATC GCTCGAG	387

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAATTCGGCC AAAGAGGCCT ACCTTCATTT GTTAGATTAT ATCAGTACCC CAACTTTGCT	60
GGACCTCATG CAGCTTTAGC TAATAAAAGT TTCTTTAAGG CAGATAAAGT TACAATGCTG	120
TGGAATAAAA AAGGTATGTT AAGTATATTT TATCCCTCCC TTTGTTTATC AGTTGTAAAT	180
TTAGGCTATA TTCCTATGTG TATAACAGAA GAATCAATGC CCATTGTGT TTTAAATCTA	240
ATTAAAGTTT TTAAGTTTAT AGCTACTGCT GTGTTGGTAA TAGCTAGCAC AGATGTTGAC	300
AAGACAGGAG CTTCTACTA TGGAGAACGA CTCGAG	336

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GAATTCGGCC AAAGAGGCCT AGGGACATTG GTTGAATTGG CATGACTAGA ATAGTTGGGA	60
ATGTTTGGGA ATGGGAGAG ATTGCTAATG GGATGTCTGC CAGGGGCAAT ACTGAAATCT	120
GCTGGTTGGT AAAGGTAGTG CCTGAGCCCA GTGCTAACCA TAGTAGTTGG AAAATTGTGT	180
ACGTTGGCTG TGGAAATCCTT ATGCGAATAT TTGTCCAATC CATCTAAATT TCTCTCTGCA	240
GCATTTTAA AAAGACATAT AGCTGAAAT TTTGTCAGTCC TAAAAATATT TTGTATTCT	300
CTGCCAGAT TTGCATTGG GTAGATCGTG CTGTAGAAGA TATATCTGC TTTAAGATAG	360
CTGCCACTGA TTAGTTTATT TTAGTCTATT TTAATCAACT TATTGCCTTG TAATCTTTCC	420
TTTTTCATTC TCTAAATTC TGAAATTCTA TCTTTCATGT TCCCCAGGAA ACACTCGAG	479

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GAATTCGGCC TTCATGGCCT ACATGATGTC AACACCGTG GCTCACAAGA TGAAAGAGCA	60
--	----

CATTCCTTTT TTTGAAGATA TGTGTAAAGG CATTAAAGCT GGTGACACCT GTGAGAAGCT	120
GGTGGGATAT TCTNCCGTGT ATAGAGTCTG TTTTGGAATG GCTTGTTTCT TCTTTATCTT	180
CTGTCTACTG ACCTTGAAAA TCAACAACAG CAAAAGTTGT AGAGCTCATA TTCACAATGG	240
CTTTTGTTT CTTTAACTT CTGCTGTTGG GGGCCATGTG CTCAGGAGCT TTCTTCATTC	300
CAGATCAGGA CACCTTTCTG AACGCCGGGC AGCTCGAG	338

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GAATTCGGCT TCATGGCCTA CCCC GAACCA CTCAGGGTCC TGTGGACAGC TCACCTAGTG	60
GCAATGGCTC CAGGCTCCCG GACGTCCCTG CTCCTGGCTT TTGCCCTGCT CTGCCTGCCC	120
TGGCTTCAAG AGGCTGGTGC CGTCCAAACC GTTCCGTAT CCAGGCTTTT TGACCACGCT	180
ATGCTCCAAG CCCATCGCGC GCACCAGCTG GCCATTGACA CCTACCAGGA GTTTGAAGAA	240
ACCTATATCC CAAAGGACCA GAAGTATTCA TTCCTGCATG ACTCCAGAC CTCCTTCTGC	300
TTCTCAGACT CTATTCCGAC ACCCTCCAAC ATGGAGGAAA CGCAACAGAA ATCCAATCTC	360
GAG	363

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAATTCGACC TTCATGACCT AGCGTAAGAG GAGAGAGACA CATTGAGCAG CCAAAGGACT	60
CGGTGGAAAG AGCAGAACAC CATAGACAAT ATGTCGCTCT TGGGACCCAA GGTGCTGCTG	120
TTTCTTGCTG AATTCATCAT CACCTCTGAC TGGATACCCC TGGGGGTCAA TAGTCAATCG	180
AGGAGACGAT GTGACTCAAG CGACTCCAGA AACATTGACA GAAGATCCTA ATCTGGTGAA	240
TGATCCCGCT ACAGATGAAA CAGTTTGGC TGTGTTGGCT GATATTGCAC CTTCCACAGA	300
TGACTTGGAG TGCTGGGATG AGAAATTAC CTGCAGCAAG GCTCTACTCT GTGCATCGGC	360
CGGTAAACT CGAG	374

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GAATTCGGCC TTCTGGCCTA GGGTGGGATA AGTGATTNGT ATTTGTTNG GTTTAAAAAC	60
--	----

```

ATACTTTGAT AGAAATTAGT CCCTTCTTT TCCTTCTCTT CTACAATGTC AATTGCCCAT      120
TTCATTTGTG TGTTCTAAC ATTTTCTTTT GTTAAGAAAT GTTGGGGCTA TAATTTTTT      180
GAAATCACTG AAGGAGGGGG AAAAATAATT TTAACAACCT GTGTTGAAAC CTTCCATAGC      240
TTAATTGACT GGAATAATCC TGCCATCATT AATAAGATGT ACAAGGTGTA CCTTGAGAT      300
ATACCACTGA AGACANAGA GGAGCTCGAG      330

```

(2) INFORMATION FOR SEQ ID NO:236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

```

TTACACCCTG GAAACCAAGC ATAAGCACAC TTTAGCAGA TGACTTAGAA ATTAAGTTGT      60
TTGAATCNAG TGAACACACT GAAGACTCCA ACAACCCACA ACTCGAG      107

```

(2) INFORMATION FOR SEQ ID NO:237:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

```

GAATTCGGCC TTCATGGCCT ACCCGTCGTT AGTGAAGGGG AAATGGGTTG TATCCTAAGG      60
GATTGGGAAA TGGGAAGTGA ATTTGAGGAG ATTGTGGAGT ACAAGGTATG TGTTTACGTT      120
AGGTGATGAG CAGTGTCAGG ATAGTGAAGT GTGGACAGTG TCAAATGCTT TTCTGTAGGG      180
AAGATGAAGT TAGCATCATC TTATCACTT TGACATGCTT TTGTGGTTTA TTTGTGTTTG      240
TATTTGTTTT TTAGTAGAAA TGAAAGGCTT TGCCAAAGCC TCTGTACTAT GCTTCAGAGT      300
AGGACACACA ATTCTGAGAT TGCTGTAGAG GGCTCGAG      338

```

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

```

GAATTCGGCC TTCATGGCCT AGTCAGAGCC AAAGGAAAGC TTGAAAAATG AAGACATTAG      60
CAGGACTTGT TCTGGGACTT GTCATCTTTG ATGCTGCTGT GACTNCCCCA ACTCTAGAGT      120
CCATCAACTA TGACTCAGAA ACCTATGATG CCACCTTAGA AGACCTGGAT AATTTGTACA      180
ACTATGAAAA CATACCTGTT GATAAAGTTG AGATTGAAAT AGCCACAGTG ATGCCTTCAG      240
GGAACAGAGA GCTCCTCACT CCACCCCCAC AGCCTGAGAA GGCCCAGGAA GAGGAAGAGG      300
AGGAGGAATC TACTCCCAGG CTGATTGATG GCTCTTCTCC CCAGGAGCCT GAATTCACAG      360
GGGTTCTGGG GCCACACACA AATGAAGACT TTCCAACCTG TCTTTTGTGT ACTTGATAAA      420

```

GTACCACCGT GTACTGTGAT GCCCATGAAC TCGAG

455

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

```

GAATTCGGCC AAAGAGGCCT AGGGGGGTGA TGGTGTGTGC TTTGGACTGT GTGCCTACAG      60
GGTTTTTTTG TTTTGTTTTG TTTTACTGTA ATGGAAATGG GTTTAGGATA AGCATACTCA      120
AAGCTCCACA GTGTATCCTT GAGCTTTCCA TGACTGCCAG TTACACACTG GAGAGGGTTA      180
AATGAATCTT AAAGTGTTCA TGATTACTAT TAAATATCAT TATAAAACAA ATTCTTTCGG      240
GGGGGCACAA ATGCTAATAT GTACAAGAAA ATCTTAGACT TGAAAATATC TTTAAAATGA      300
AAATAACTTT TTTTTCAGC TGACTGTATT CACAACCTTG ATGGATGTTA CCAAAGGTCA      360
ATTTGAAAGT CACCTTCGAG ATTGCCCGA CCCTGTGATA GGCTGGTGAG CACACGTTGG      420
CCAGCCTCGA G                                     431

```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

GAATTCGGCC TTCATGGCCT ACTACAATCC GTGGGTGCTC NTTCTTGCCT ACTTTACTCT      60
CCCACTGAAG CAGGTTANCG TTGAAGGTGG TATGGAAAAG CCTGCATGCC TGTTCATTC      120
TTTTGTTTCT TCTCCTTCCC CCTCCCCCTA CCTCCTTCCC CTACCTCCTT CGTCCGAG      178

```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

GAATTCGGCC TTCATGGCCT ACATCAACAG CATCAAGTCC AGACTAAGCA AAAGTGGGCA      60
CATACAACT CTGCTTAGAG CATTGGAAGC TCGTGATCGA AACATACAAG AAAGCAACTT      120
TGATAGAGTC AATTCTGGT CTATGGTTAA TTAGTGGTC ATGGTGGTGG TGTCAGCCAT      180
TCAAGTTTAT ATGCTGAAGA GTCTGTTTGA AGATAAGAGG AAAAGTCTCG AG          232

```

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```
GAATTCGGCC TTCATGGCCT ACAAACCTA ACTTCGCAG AAAACAAGAT GAGATTGGCA    60
TGGCTTTATT TGTTTTTTT GTTTGTTT GGTTTTTTT TTTTTTTGG CTGACTCAG    120
GATTTAAAAA CTGGAACGGT GAAGGTGACA GCAGTCGGTT GGAGCGAGCA TCCCCAAAG    180
TTCCTGCGGC TCGAG                                         195
```

(2) INFORMATION FOR SEQ ID NO:243:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```
GAATTCGGCC TTCATGGCCT ACATATCCTC AAATGGTAGT CATCTGGGGA CTAAGCAACA    60
GGTGTTCCTAA GGAACCTAAT CTCTGGGTTT GAAAAGTTCA CAGTCTGTGC AGTCTATTCG    120
TCCTCCATAT AACCGAGCAG TGTCTCTGGA TAGCCCTGTT TCTGTTGGCT CAAGTCCTCC    180
AGTAAAAAAT ATCAGTGTCT TCCCCATGTT ACCAAAGCAA CCCATGTTGG GTGGGAATCC    240
AAGAATGATG GATAGTCAGG AAAATTATGG CTCAAGTATG GGAGACTGGG GCTTACCAAA    300
CTCAAAGGCC GGCAGCGGAC TCGAG                                         325
```

(2) INFORMATION FOR SEQ ID NO:244:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 342 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```
GAATTCGGCC TTCATGGCCT AGGAGGCTAT TTAGGATTT CAATGAGAAG CAAAATCATA    60
TCCAAATCAA AGTAAAGGTC ATCGGTGGCC AATGAAGAGC GGAGAAAACG GAGGCGGGAG    120
AACAGACGCG ACCTCAAGAC AGAAGAATGG AAGACGCAAC TTTCAAGAAA AGAGGAACTG    180
AAACGAAAAG AGAGGCACAG TCCAAATGAG GAAGAGAACA AGGAGCCTTC AGTCTCCTGG    240
GGGCCAGGGA GCCTCGCCAC GCGGTCACAG GTACACGGGG ACATTAGAG GCCATCTCCT    300
TTAAAGCCAG ACATTCTTCT TACTGGAATC TAGGCCATGA AG                                         342
```

(2) INFORMATION FOR SEQ ID NO:245:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GAATTCGGCC	TTCATGGCCT	AGGCGGGTGA	CATTCAGCCG	GCGGTTGGG	GGGACGGANT	60
CTCCATTCCA	GAACCATGGC	CCAATTTGTC	CGTAACCTTG	TGGAGAAGAC	CCCGGCGCTG	120
GTGAACGCTG	CTGTGACTTA	CTCGAAGCCT	CGATTGGCCA	CATTTTGGTA	CTACGCCAAG	180
GTTGAGCTGG	TTCCTCCAC	CCCTGCTGAG	ATCCCTAGAG	CTATTAGAG	CCTGAAAAAA	240
ATAGTCAATA	GTGCTCAGAC	TGGTAGCTTC	AAACAGCTCA	CAGTTAAGGA	AGCTGTGCTG	300
AATGGTTTGG	TGGCCACTGA	GGTGTGATG	TGGTTTATG	TCGGAGAGAT	TATAGGCAGG	360
CGGGTCACTC	GAG					373

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAATTCGGCC	TTCATGGCCT	AAACAGGACC	TGCTTCACAC	CACCAAGCAT	CAGGATGTGT	60
TGCTCAGTGA	GCAGACCCGA	CTCCAGAAGG	ACATCAGTGA	ATGGGCAAAT	AGGTTTGAAG	120
ACTGTCAGAA	AGNAGAGGAG	ACAAAACAAC	AACAACCTCA	AGTGCTTCAG	AATGAGATTG	180
AAGAAAACAA	GCTCAAACTA	GTCCAACAAG	GAAATGATGT	TTCAGAGACT	CCAGAAAGAG	240
AGAGAAAGTG	AAGAAAGCAA	ATTAGAAACC	AGTAAAGTGA	CACTGAAGGA	GCAACAGCAC	300
CAGCTGGAAA	AGGAATTAAC	AGACCAGAAA	AGCAAACCTG	ACCAAGTGCT	CTNCAAAGGT	360
GCTGGCAGCT	GAAGAGCGTG	TTAGGACTCT	GCAGGAAGAG	GAGAGGTGGT	GTGAGAGCCT	420
GGAGAAGACA	CTCTCCCAA	CTAAACGGCA	GCTTTCAGAA	AGGGAGCAGC	AATTGGTGGA	480
GAAATCAGGT	GAGCTGTTGG	CCCTCACGCT	CGAG			514

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GAATTCGGCC	TTCTGGCCTA	GGACTCTATA	GAACCCACTG	CCTCCTGATG	AAGTCCCTAC	60
TGTTCAACCCT	TGCAGTTTTT	ATGCTCCTGG	CCCAATTGGT	CTCAGGTAAT	TGGTATGTGA	120
AAAAGTGTCT	AAACGACGTT	GGAATTTGCA	AGAAGAAGTG	CAAACCTGAA	GAGATGCATG	180
TAAAGAATGG	TTGGGCAATG	TGCGGCAAAC	AAAGGGACTG	CTGTGTTCCA	GCTGACAGAC	240
GTGCTAATTA	TCCTGTTTTT	TGTGTCCAGA	CAAAGACTAC	AAGAATTTC	ACAGTAACAG	300
CAACAACAGC	AACAACAAC	TTGATGATGA	CTACTGCTTC	GATGTCTTCG	ATGGCTCCTA	360
CCCGTTTCTC	CCACTGGTTG	AACATTCCAG	CCTCTGTCTC	CTGCTCTAGG	ATCCCCACGC	420
TCGAG						425

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAATTCGGCC TTCATGGCCT ACAAAGGAA AGAAGAAAAA GGGCCAAAAG CCAAATGAA	60
ACTGATGGTA CTGTGTTTCA CCATTGGGCT AACTTTGCTG CTAGGAGTTC AAGCCATGCC	120
TGCAAATCGC CTCTCTTGCT ACAGAAAGAT ACTAAAAGAT CACAACTGTC ACAACCTTCC	180
GGAAGGAGTA GCTGACCTGA CACAGATTGA TGTCAATGTC CAGGATCATT TCTGGGATGG	240
GAGGGGATGT GAGATGATCT GTTACTGCAA CTTTCAGCGAA TTGCTCTGCT GCCCAAAGA	300
CGTTTTCTTT GGACCAAAGA TCTCTTCGT GATTCCTTGC AACAATCTCG AG	352

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GAATTCGGCC TTCATGGCCT ACACAATGGT GTTCGCATTT TGGAAGGTCT TTCTGATCCT	60
AAGCTGCCTT GCAGGTCAGG TTAGTGTGGT GCAAGTGACC ATCCCAGACG GTTTCGTGAA	120
CGTGACTGTT GGATCTAATG TCACTCTCAT CTGCATCTAC ACCACCACTG TGGCCTCCCG	180
AGAACAGCTT TCCATCCAGT GGTCTTTCTT CCATAAGAAG GAGATGGAGC CAATTTCTAT	240
TTACTTTTCT CAAGGTGGAC AAGCTGTAGC CATCGGGCAA TTAAAGATC GAATTACAGG	300
GTCCAACGAT CCAGGTAATG CATCTATCAC TATCTCGCAT ATGCAGCCAG CAGACAGTGG	360
AATTACATC TGCATGTTA ACAACCCCCC AAGACTCGAG	400

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GAATTCGGCC AAAGAGGCCT AAGAGATTCA GGACCTGCAG AGTCGCCAGA AGCATGAAAT	60
TGAATCTTTG TATACTAAAC TGGGCAAGGT TCCCCCTGCT GTCATTATTC CCCAGCTGC	120
TCCTCTGTCT GGGAGAAGAA GGAGACCCAC TAAAGCAAA GGCAGCAAGT CTAGTCGCAG	180
CAGCTCATTG GGCAATAAAA GCCCAGAGCT TTCAGGCAAC CTGTCTGGTC AGAGTGGAA	240
TTCACTCTTA CACCCCAAC AGACCCTCCA CAGTCGAG	278

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GAATTCGGCC TTCATGGCCT AGTTTATATA CTTTCTCTGA AGGATCCTAA TGATAGTTAA	60
CCATTTCTCA TTTTATTTT GCTGGATTGT TTTCTGTTT TGCTTCAGC ATTCTTGCTT	120
TGCTGTGCT TACTTTTGA GTTTTGATTC CCTGTGTCAC TGTTTTCTT CGCATCCACC	180
ACTCGAG	187

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GAATTCGGCC TTCATGGCCT ACTTCTCTGG AAAGGTCAC GATTGTTGT TTTTCGAGA	60
CAGGGTCTCG CTCTTCACCC AGACTGCAAT GCAGTGGCAC AATCATAGCT TATTGCAACC	120
TCAAACCTCGT GGGCTCAAGC AATGCTCGCT CCTCCCAAGT AGCTAGGACC ACAGGCATGC	180
ACCACGATGC CCACCTAGTT TTTTGTATTT TCTATAGAGA NGGGGGTCTC ACTGTGTTTC	240
TCAAGCTGGT CACATACTCT TGGCCTCAGG CAGTTCTCCC ACATCAGANT CTCAAAGCAC	300
TGGGCTTACA GCTGNGAGCC NGNCCTTTT AAAAAAAAAA AAAAAATCAA AACAAAACAA	360
AACAAGATTA TGTCTTTCCC ACGCATCTCG AG	392

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GAATTCGGCC TTCATGGCCT ACTTGGGAAT TAACATCTTC GATAAATCCC AGAAGTCTTT	60
AAGTGACAGT AGAGAGCCTA CAGAGAAGCC TGGGAAAGCA GAAAAATCTA AGAGCCCAGA	120
AAAAGTGTC TCGTCTCAA ACTCCTCCTC CAACAAGGAA TCAAAAGTAA ACAATGAGAA	180
GTTTCGTACT AAGAGCCCCA AGCCTGCCGA AAGCCCCCAG TCAGCCACTA AGCAGTTGGA	240
TCAGCCCACT GCTGCTTATG AGTATTATGA TGCTGGCAAT CACTGGTGCA AAGACTGCAA	300
CACCATCTGT GGGACTCGAG	320

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

```

GAATTCGGCC TTCATGGCCT AATCAGAAGC TTTTCAAAAT TCCGTCTTCA AGAAGAAACA      60
CCCGTGGAGG AAGAAGACAT TATACAAAAC AAATTTAGAA ACTGGGATCA TGAGTGGAAG      120
AACAAAGGCA AGAAGGGCTG CCATGTTTTT TAGACGTTGC TCTGAAGACG CCAGCGGTAG      180
CGCCAGTGGC AATGCTTTGT TATCAGAGGA CGAAAATCCT GATGCGAATG GGGTAACTCG      240
ATCATGGAAG ATTATTCTAA GTACAATGCT TACACTGACT TTTCTTCTTG TAGGACTCCT      300
AAATCATCAG TGGCTTAAAG AAACAGATGT TCCTCAGAAA TCCAGACAAT TATATGCCAT      360
GCTCGAG                                           367

```

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

```

GAATTCGGCC TTCATGGCCT AAAGTAGTTC TGTTATAAAA AGCCAGGAAT CCTAAAACCA      60
AAATATTAGA ACGAAAACAG AAACATGGCT CACTATATTA CATTTCTCTG CATGGTTTTG      120
GTGCTGCTTC TTCAGAATTC TGTGTTAGCT GAAGATGGGG AAGTAAGATC AAGTTGTCGT      180
ACTGCTCCGA CAGATTTAGT TTTTCATCTTA GATGGCTCTA ATTGTGTTGG CCCAGAAAAC      240
TTTGAAATAG TGAAAAGTG GCTTGTCAT ATCACAAAAA ACTTTGACAT AGGGCCGAAG      300
TTTATTCAAG TTGGAGTGGT TCAATATAGT GACTACCCTG TGCTGGAGAT TCCTCTCGGA      360
AGCTATGATT CAGGAGAACA TTTGACGGCA GCAGTGGAAT CCATACTCTA CTTAGGAGGA      420
AACACAAAGA CAGGAAGAA CCTCGAG                                           447

```

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

```

GAATTCGGCC TTCATGGCCT AAATGAAGCA AAATTCCATA CATCATTTTG AAAATAGTGT      60
TTCTTTCCCT GATAGGCCTG TTCTGCATCA TTCTTTTAGC TTCCTTCTGC CCTGTTTATC      120
ACTTGGTCCC ACTTTTATAT TTTTCTCTT CGTCCAGAA TTTCTATTT AGTTTCTGT      180
ATTTGCTTA CTCCCTCCCT TCTCCATGAT TCAGCCTAGT CTTTCCGTCC TCTGTGGACT      240
TGGGTGTGCC TTCCTCTGGG CCACCTCGTC TTTTGCTGCT GTTAGCCCTC CCGCCTGCGC      300
ACCTGCCACT TCACCCTCGC CTGTGGTCCA CTTACGTTCC ACTCAGCCCG GTCAGTCCTG      360
CTTTGTTCTT CTCCACCGCC TAGGTCTCGA G                                           391

```

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GAATTTAAGT TCCAGTATGA GATCTTCAAA GCTGTCTTTT TTTTTCTTC TTCCGTTCTC	60
AGATCCTGAG	70

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

GAATTCGGCC AAAGAGGCCT AGTCAAATTC TTACCTCGCT CTTTCACTGC TAGTAAGATC	60
AGATTGCGTT TCTTTCAGTT ACTCTTCAAT CGCCAGTTTC TTGATCTGCT TCTAAAAGAA	120
GAAGTAGAGA AGATAAATCC TGTCTTCAAT ACCTGGAAGG AAAAACAAAA TAACCTCAAC	180
TCCGTTTTGA AAAAAACATT CCAAGAACTT TCATCAGAGA TTTTACTTAG ATGATTTACA	240
CAATGAAGAA AGTACATGCA CTTTGGGCTT CTGTATGCCT GCTGCTTAAT CTTGCCCCTG	300
CCCCTCTTAA TGCTGATTCT GAGGAAGATG AAGAACACAC AATTATCACA GATACACTCG	360
AG	362

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GAATTCTAGA CCTGCCTCGA GTGCGGATCC AGCCGGAGGC GAAGAGAAGC ACTTTGGGGG	60
CAAAAGAAGA GAAAAATGAA GACGGGACAT TTTGAAATAG TCACCATGCT GCTGGCAACC	120
ATGATTCTAG TGGACATTTT CCAGGTGAAG GCTGAAGTGT TAGACATGGC AGATAATGCA	180
TTTGATGATG AATACCTGAA ATGTACGGAC AGGATGGAAA TTAAATACGT TCCCCAACTG	240
CTAAAGGAGG AAAAAGCAAG CCACCAGCAA TTAGATACTG TGTGGGAAAA TGCAAAAGCC	300
AAATGGGCAG CCCGAAAGAC TCAAATCTTT CTCCCTATGA ATTTTAAGGA TAACCATGGA	360
ATAGCCCTGA TGGCATATAT TTCCGAAGCT CAAGAGCAAA CTCCCTTTTA CCATCTCTTC	420
AGTGAAGCTG TGAAGATGGC TGGCCAACCTC GAG	453

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GAATTCGGCC TTATGGCCTA CTTTAAAAAA AAACCAATAC CAAAGAAGCC TACAATGTTG	60
GCCTTAGCCA AAATTCTGTT GATTTCAACG TTGTTTTATT CACTTCTATC GGGGAGCCAT	120
GGAAAAGAAA ATCAAGACAT AAACACAACA CAGAACATNG CAGAAGTTTT TAAAACAATG	180
GAAAATAAAC CTATTCTTTT GGAAAGTGAA GCAAACCTAA ACTCAGATAA AGAAAATATA	240
ACCACCTCAA ATCTCAAGGC GAGTCATTCC CCTCCTTTGA ATCTACCCAA CAACAGCCAC	300
GGAATAACAG ATTTCTCCAG TAACTCATCA GCAGAGCATT CTTTGGGCAG TCTAAAACCC	360
ACATCTACCA TTTCCACAAG CCCTCCCTTG ATCCATAGCT TTGTTTCTAA AGTGCCTTGG	420
AATGCACCTA TAGCAGATGA AGATCTTTTG CCCATCTCCC TCGAG	465

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GAATTCGGCC TTCATGGCCT AGCGGCGGGG CGAGCGCCTC CACGCAGCAA CTCCGGAGTC	60
CCCCGCTTGC CCGAGCGCAG TTTCTCCGCT GCTGTTTCCA CCGGCTTTGT AACACTGGGA	120
ATTTACATCC TCACCCGCAC CCTCAGGCC CGAGGATTTT AAACCTACCT TTACTCTCGA	180
ACTGAGAGTT GCGGTAGATG GGATTTTTC CTTTTCCCA GATGGTTGAA GGTTAAGATT	240
TTTGGAACCC CCCCCACCTC CTTATTTCTA TTATTATTTT TGCNAGAAAA GTATAAAGAG	300
AGTTGTAGTG GAGGTGAGAT TTGTGATCGG GAAAGCCTTC GACTCCCTCC TTCTCCGTCT	360
TCCGCTTCTC TCTCTCTGAT TAGTTCCTAT CCAGCAGCAG ATTGAAGCAG GAGATGATTC	420
TTCTCAAGGT TTGTTTCAGCA GCTTCACTTC TAGGCGAAGG CTTTCATGAAC CAAGTGACGA	480
ACAACCTCGA G	491

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GAATTCGGCC TTCATGGCCT ACATTTTCT ATTGATATAA AAATTGTTAG AGAAATATAC	60
AGTTGTATAT TTCCCCCTT TATACAGAAA TTTTACAATA ATTTTCAGATT TTTCTGAGTT	120
TTTTCAGATT TTTGATTCTA TAATATGAGA TTATCTTTC TTCCTCTTAT TTTTTAGGT	180
TATTTATTTT TTCTTTTCTT TTTAATTTGC TCATACAGGT TTAATCTCGA G	231

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GAATTCGGCC	TTTCATGGCCT	AGTAAAATTT	AAAATACATA	CTAACATATA	ACCCAATTTT	60
AACATATTAA	GTGAATATGT	ATTCTTAAAA	GATCCACTAC	TTTACATTTA	GATGCGTTAG	120
GATGTATTAG	AAATAAAAAC	AGAAGAAAAG	ATTTAGAATC	TAGTCTGTCT	TTGCCACTCA	180
AGCTAGTTAC	CCTCTCTGAG	TTTTATACCC	CCTTCATCTA	TTAAAATGGG	GGGTAACGCC	240
AACCTGACTC	CTTTAAAATG	AGTTTGAGAG	TCAGGC AAAAT	TAGAAAAGATA	CATAGATGAA	300
AAC TTTTAA	AAAGTATATA	GTCTTTCATG	ATTTGTAGAA	CACTTTTATA	CTTTTCAGAG	360
TACTTTCACA	TTGATCATAT	TGTTTG TACT	TTATGAAAGT	CTTCTACAAA	TCAGAATTAT	420
GCTTATTATA	CAGATGTGGC	TCGAG				445

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 343 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GAATTCGGCC	AAAGAGGCCT	AATTACTTTA	TATTTTAAAA	GCTCTGTGAC	TTCAGTAGTG	60
CATTGAAATA	AAATTTTAT	TCATTATGAG	AGAGTCTGTG	AGGAACAGAA	TCATGGTTCC	120
TGTGTGTTTG	AAGATATGGC	GTGGGGTGAT	AGTGCTGGCA	GCAGCTCTGT	TGCTCTTG TG	180
CCCATGGCAT	ACAGACTGGA	TCTGCTGGTC	CACGGCTCCT	GAGGTTAATG	TCCAAGCCCT	240
CTGCAATGCT	GACAGTCTTC	CTCATCCTCA	CACCCTACCT	CTCAGTTTCT	ACCTGCCACC	300
TCCCCAGTAA	TATTAGCCTC	TTGAGTCCCC	AACAACACTC	GAG		343

(2) INFORMATION FOR SEQ ID NO:265:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GAATTCGGCC	AAAGAGGCCT	ATTAAAATTC	ATTTATCAGT	AGGATCATTC	TGTTCTAGAC	60
AAGTTGGCTA	TATTATAAAA	CATTAAAGCA	GCAGGCACTA	AGTTAAATAT	TGTAGCAGTT	120
GAAATTTAAT	GCTAATCTTA	CAGTTT TACA	CAGTTAACAA	TCTAGGCCAA	ATCTATTGAT	180
ACCTTTGGAA	CTACCCTTTA	AATTCCATCC	TATGCTTG TG	AAAAGGTTGC	ATATAATTTT	240
TTTTCTTTT	TCTCTCTTCT	CTTCCTCTTC	TTTTTTCTTT	TTCTTTTCT	ATTTCCCTTT	300
TCTTCCTTTT	TCTTTCACAG	AGTCTTG GTA	TATCACCCAC	ACTCTCGAG		349

(2) INFORMATION FOR SEQ ID NO:266:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 335 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

```

GAATTCGGCC AAAGAGGCCT AGAATAAAAA TGCTTGTGTC AAAAAATCAA ACATTTGTCT      60
CTTTCCTTTC CATTCCAGTT CTAGGTCTCG TTCCAGATCA TATTCTCCAG CTCATAACAG      120
AGAAAGAAAC CACCCAAGAG TATATCAGAA TCGGGATTTC CGAGGTCACA ACAGAGGCTA      180
TAGAAGGCCC TATTATTTCC GTGGGCGTAA CAGAGGCTTT TATCCATGGG GCCAATATAA      240
CCGAGGAGGC TATGGAAACT ACCGCTCAAA TTGGCAGAAT TACCGGCAAG CATACAGTCC      300
TCGTCGAGGC CGTTCAAGAT CCCGGCTCCC TCGAG                                     335

```

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```

GAATTCGGCC AAAGAGGCCT AGTGGAAATT TGTGGCTAGT GTGATTTTGG TTTGTTTCCT      60
TTTAAGTACT GTTGATCAGT TGTGACACTT ACTGGTTAAA CTTACGTTGC TAAAGATTTC      120
TCTATAATAA GCCACACATT ATATTTAGAC TATATTAAGG GACCTTGTTT TTCTTCTAGA      180
TAGCAGCTGT CCCAAAGAAA ATATTTCTTC TTTGTCTGTT AAGATTTAGC TATTATCTGC      240
CAGTTGTAA GAGGTTTTGG TTCCAACTC AACCAGCAAT GTTGAGAGCT GAACTTAAGA      300
TAGCTGTTGT ACTTTTGTCT TTCCATCTGT TACTGTCCTT CATTCTGGC TCCCTACTAT      360
CTATAAACAG CAAGCTCGAG                                     380

```

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

```

GAATTCGGCC AAAGAGGCCT ATCTAGACCT GCCTCGAGTC AGCAACAACA ATTTTAAAAA      60
TTTCTTTCTG GATTCTAGAG TGAGTTTTTT TCATAACACA AGAGGATAAG AGTGAGGACA      120
ACAGGAGGTA TTGATGATCT GCTGAGCACC AGGCATTATG CTAAGTGCAT TCACACACAT      180
CTCAGTGCCT ATTGCCTCGT TGTGGACTTC TCTATCCCAG CTCGTCCCCC TGGCAAATTC      240
TTTCTCATCC TTCAACTCTC AGACACCTCC CCCGCGCCTC GAG                                     283

```

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

```

GAATTCGGCC AAAGAGGCCT AACCAGGCAT TTTTCATTAG GGTTCTAGGT CCAGGTGAAT      60
TCTTGAGTTG GTTCGTTGTG TCATGIATTG GCCTTTAATA ATGCTCTTAT TTTGGCCAC      120

```

GCCTGTGGTC CCAGCACTTT GGGAGGCTGG TCTCGAG

157

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GAATTCGGCC AAAGAGGCCT AACCAGGCAT TTTCATTAG GGTTCAGGT CCAGGTGAAT 60
 TCTTGAGTTG GTTCGTTGTG TCATGTATTG GCCTTTAATA ATGCTCTTAT TTGGCCCCAG 120
 GCCTGTGGTC CCAGCACTTT GGGAGGCTGG TCTCGAG 157

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GAATTCGGCC AAAGAGGCCT ACCCAAATAA AATCAGAGTC AGAAATGGAA ACAGACAGTG 60
 GAGTACCTCA AAACACTGGA ATGAAAAATG AAAAAACAGC CAACAGGGAA GAGTGTGCGA 120
 CCCAGGAGAA AGTTAATGCA ACAGGACCAC AGTTCGTGAG TGGAGTGATT GTGAAGATCA 180
 TTAGCACAGA GCCTCTACCT GGCAGGAAAC AAGTCCGGGA TACTTTGGCA GCAATCTCAG 240
 AAGTTCTTTA TGTTGATTG CTAGAAGGGG ATACAGAATG CCATGCTAGA TTTAAACTC 300
 CTGAGGATGC TCAAGCAGTA ATAAATGCCT ATACAGAAAT TAACAAGAAA CACTGCTGGA 360
 AACTCGAG 368

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GAATTCGGCC AAAGAGGCCT ACAACGAACG GCTTGGGNGC GGACTGGTAT CCGGGGACTG 60
 TGACTTGCGAG GGTCCGCCAT GGAGCCAGAG CAGATGCTGG AGGGACAAAC GCAGGTTGCA 120
 GAAAATCCTC ACTCTGAGTA CGGTCTCACA GACAACGTG AGAGAATAGT AGAAAATGAG 180
 AAGATTAATG CAGAAAAGTC ATCAAAGCAG ANGGTAGATC TCCAGTCTTT GCCAACTCGT 240
 GCCTACCTGG ATCAGACACT TGTGCCTATC TNATNACAGG GACTTGCTGT GCTTGCCAAG 300
 GANAGACCAC CACATCCCAT TGAATTCTA GCATCTTATC TTTTAAAAA CAAGGCACAG 360
 ACTCGAG 367

(2) INFORMATION FOR SEQ ID NO:273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

```
GAATTTGGGT CCTAGGATAT AAATATTTT CCCTTTATAA GATATTTATA GGATATTGCA    60
AACAATTCT GTTTTTCAT ATCCTTGCCA GCAGTTAGGG TTATCAAATT CTTTGATTTC    120
TTACTGATT GTAAGTTTT TTGTTTGT TTAGGTATT TCAGGATAGT TACAAATGTT    180
AGGAAACTT ATTTTATTT GGCTTTTGAA GTTCCAGAT TTCTGAACA GTGACCAATA    240
TGGACTCGAG                                         250
```

(2) INFORMATION FOR SEQ ID NO:274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

```
GAATTCGGCC AAAGAGGCCT ATCTTTTTC CTCTTTTTT GTTGCGAGAA TGATAACCTA    60
CTATTCATA TTCTGTGCCT TGCTTTGTT GCATACTGAA AATTATCCAT GGAAGGATAC    120
AGCACCACTC GAG                                         133
```

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

```
GAATTCGGCC AAAGAGGCCT AATGAAACAT TTCTGTAACC TGCTTTGTAT CTTGATGTT    60
TGTAATCAGC AAAGTGTATG TGACCCGCCT TCACAAAATA ATGCAGCAA TATTCCATG    120
GTTCAAGCTG CTTGAGCAGG ACCCCATCT CTGAGAAAAG ATTCGACTCC AGTTATAGCC    180
AATGTAGTAT CATTGGCAAG TGCCCTGCT GCTCAGCCTA CAGTGAATC TAACAGTGTC    240
TTACAAGGTG CAGTTCCAAC AGTAACAGCG AAAATCATCG GTGATGCAAG TACTCAAACA    300
GATGCCCTGA AACTGCCACC TTCCAACCT CCAAGGCTTT TGAAGAACAA AGCTTTATTA    360
TGCAAAACCA TCACACAGAC TAAAGCCACA CTCGAG                                         396
```

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

```
GAATTCGGCC AAAGAGGCCT ACCCCTCCCC ATTTCTAGTT TCATGAACTG TGCACAGGGA      60
TATGGGGCTG TTCGAGGTAC TTTTGGGCTG ACCAAGGCTC AGAGGCTACT GACAGCTTTG      120
CTGCAAGTAA CTTCTAGGCC TTGTGGGTCC CAGTGCAGGG AACCCATGTG CCGTGACACT      180
GGAGAAGCCA TCTGATCCAG GTCTCTCACT TGACAGATGG GGAAACTGAG GTCCAAAGAG      240
GTACAGCAGC TTGGTTTAAG AGATAGAGAT GGAAC TGGA CAAAAATAAT AACCATTTGA      300
TAATATTTTA ACATTATTG ATTTGTTTTT ATATGCCAAG ACCTTTTAAA GCATTATCTC      360
CTTTAAACTC TCATAACCAC TCTTACTCGA G                                     391
```

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```
GAATTCGGCC AAAGAGGCCT ACTGCTTCCT GATCATTGT CTTTTTAAAT AAAAATATGA      60
TATTTGAGAT TCTTTTATTC TCTTTAAATA TTTGAATACA GAGTCTATTT GAAGGACCAG      120
TATATTGAAT AGCAGTAATA TTTGAAGGAC TAGTCAGCTG TAGAAGCCTT GACTTCAGAT      180
CTTCAACCAA GAAACTCTGT GTATTTGCTT TTCCTGGGCC ACTCAGATAG ACAATTGTGT      240
TTTGATACA GTAAGAGTTT GCAGCTTAGC TTAAC TAGAA ATAATCCGGA TGCTCGAG      299
```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```
GAATTCGGCC AAAGAGGCCT ACTAGGATTT GAGGAGGACG CCTCTTTTGC AGGAGGATGC      60
AGTGAACAGC CAAAGTCATC TGACATCCTT TTCCATCTTT TTCCTTCTAG TATCCCAGTT      120
TCAAGGCCCA GGAAAGGCAG GACTAACAT ATGGAGCAGT TACCCAGAG TTCAAAGGGT      180
TAATCTCTAA GAATTCATTC TCTGACACCA GCCACAGCTC TTGTCCCCAT CTCTGGGACC      240
GTCCCCCTCT AGCCCCAGGT TGGCAGCTTC CCTGAATTCC TTCTATGATA TAATTGTGTA      300
TTCGGCAGGG CTCTGGGACC CAGGCTCAGA GACCCAGGCT CTGCTCTCTC CTCAGTTTCC      360
AGGAGTCAGG GCTTGCTCTA AGGGAGGAAG TAAACAGGCC TTTCCCTTGC TCCCTCTCCT      420
TTTCCTCGAG                                     430
```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GAATTCGGCC	AAAGAGGCCT	AGTGGGAGTT	AGATGTATTA	TATAAAAATG	TCCCCAGCAT	60
CAAAATGACT	CAGAGTATGA	CTGTATTTTT	AAATTAAATA	TCAAGACCTA	TCATCTGACA	120
AAACATATGA	ATGACAATGA	GATATAATAT	TTGAAATTAG	ATCCGTTCTG	GGGAATCAAA	180
GATATTTTGT	AACAGTATAC	ACAGTAGGCA	TTGGTAAGTA	AATGAGAACT	CTATGAGCTG	240
TTTTCTGGAA	AAGTTTAAAA	TGAAATTTGT	CAAATATCAA	ATGATTGTTA	TAAGAAAATC	300
AGTGGAGGCA	GTATCCTTGG	AAAAATCCAG	AAACAGTTTT	GTNTGTTTGT	TGTTTTTTAC	360
ATCAAGGCAG	ATCAGCAGGT	GAACAGCTCG	AG			392

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

GAATTCGGCC	AAAGAGGCCT	AGAAGAAACT	TTTTCTTGGG	AGCAAGGTAG	TTATTTCAAA	60
GCACAGAAAA	AGCGGCGGG	GGGCACAGAG	AAGCACAGAG	AAGCGGGGGC	AGTTGCTCAG	120
GTAAAACATT	CATCTTGGCT	TTTCTTTTTA	AAAGATAAAC	TTTGTCCAC	GTAAAGAGGA	180
AAACTGCATA	GATATTCATT	GAGATTATCT	GATTTGTCAC	TGTTGCCAAA	GAAAAAACAA	240
AGGTAATAA	CACGAGTTTC	TGCATTGAGA	AGAAAGTATT	TCAGGTAAAA	ATTAACATT	300
AAGCAACTTT	TCTCAGCAGA	AGAAATGCCC	AAATCTTAA	GGACAGTACT	CGAG	354

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GAATTCGGCC	AAAGAGGCCT	ACTTTGAGAT	TTTTTTGTTG	TTGTTTCCTT	TTTGATTTT	60
ACTGATATCA	CCAGGATAGT	TTACTCTCCT	TCTAGCTTTC	TGCTTACCGC	ACACTGGATG	120
ACACACACAT	ACACACCCGC	AAAAATGCTC	ATGAACCCAA	TCCGGAGAAG	GTTCCAGCAG	180
GTCCCCCACC	CTCCCCCTCT	CGTCCTACTT	CTCCTCTTGA	CAGCGAGGAC	AGGAGGGGGA	240
CAAGGGGACA	CCTGGGCAGA	CCCGCCGGGT	CTCCCCCACC	CCCACCCGGC	CCTCANATCA	300
TACTCGAG						308

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GAATTCGGCC	AAAGAGGCCT	AGACCTGCCT	TGTGTTTTCC	ACCCTGAAAG	AATGTTGTGG	60
CTGCTCTTTT	TTCTGGTGAC	TGCCATTTCAT	GCTGAACCTCT	GTCAACCAGG	TGCAGAAAAT	120
GCTTTTAAAG	TGAGACTTAG	TATCAGAACA	GCTCTGGGAG	ATAAAGCATA	TGCCTGGGAT	180
ACCAATGAAG	AATACCTCTT	CAAAGCGATG	GTAGCTTTCT	CCATGAGAAA	AGTTCCCAAC	240
AGAGAAGCAA	CAGAAATTTC	CCATGTCCTA	CTTTGCAATG	TAACCCAGAG	GGTATCATTC	300
TGGTTTGTGG	TTACAGACCC	TTCANAAAAT	CACACCCCTC	CTGCTGTTGA	GGTGCAATCA	360
GCCATAAGAA	TGAACAAGAA	CCGATCAAC	AATGCCTTCT	TGTAAANGA	CCAAACTCTG	420
GAATTTTAN	AAATCCCTTC	CACACTTGCA	CCACATCTCG	AG		462

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

GAATTCGGCC	AAAGAGGCCT	AGCAGATTCT	TAATTTCCCT	GTCCATATTT	TCCCCTTTCC	60
TTTCTCCCTG	CCCGTTCCAT	GGTCTTATCT	GGCTGCTTTC	TCAATTTATT	CTTGTTTGCT	120
TGTGGATTCC	CTTCTATTAA	TCTTGAAGTC	GTTACTGACA	TGTTTGGCCC	TATACCAGCT	180
AGACCATTGC	CTGAAGACTT	TTTGATGAAC	AATCTGTGTA	AAGAAAAGG	GAATCTCGAG	240

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

GAATTCGGCC	AAAGAGGCNT	ACCAGGANTT	TCTATTCAAT	TGAGAAGAAC	CCAGCAAAAT	60
GGGGATCTCC	ACAGTCATCC	TTGAAATGTG	TCTTTTATGG	GGACAAGTTC	TATCTACAGG	120
TGGGTGGATC	CCAAGGACTA	CAGACTACGC	TTCAGTGATT	CCCTCGGAGG	TGCCCTTGGA	180
TACAACTGTA	GCAGAAGGTT	CTCCATTTC	CTCGGAGTTG	ACCCTGGAGT	CAACTGTAGC	240
AGAAGGTTCT	CCGATTTCCT	TGGAGTCAAC	CCTGGAGTCA	ACTGTAGCAG	AAGGTTCTCT	300
GATTCCCTCA	GAGTCAACCC	TGGAGTCAAC	TGTAGCAGAA	GGACTCGAG		349

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GAATTCGGCC AAAGAGGCCT AAAAAAATAA GAAATAATCT ATTCCACATT TAATAATTTG	60
AATCTTCCTG CTATAGATAT TTGGTTATCT TGACTTTTIA ANATAACATA TTTCTACAGG	120
ATTTTGAGTC TGAGAAGAGA AAGGTAANAT GCAAGACACT TCGATTTGTT GCACATTATT	180
ATGGAGCATC ATTAATGGTT TGNACATTTC TTGTCCTTTG GGCTTGAATG GACAGTACCA	240
AATTTGGGGT AATCAGCAAC TTGATGCACA GCTACGAGGA ATAAATGCTT TTGCTAATGC	300
ACTCGAG	307

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GAATTCGGCC AAAGAGGCCT AAAAGATTAA AAAAAAATTT GTGTGATTTG ACTATATATT	60
AAAATCTCTT TCATAATTAG TCAACAATTT AAGCAACAAT TAAATTATTA GTGCTGTGGA	120
AAATATAGAA GAAAGATAAT TTCTTATCC CCTCCTGAGG AAAGCATTG ATACACCTGG	180
AAAGGAGCTG CTATGAAGCC AATTTATCTG TTCTTTTAT CAATTCAGCA GCATTTAAGA	240
TCAGATTTT TCTCTAGTGG TCCAGCAGAG GGAGCCCTAG CACATGAATT GTTTTCATTT	300
CGTGCTTGCA CCCAGGATCT CGAG	324

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

GAATTCGGCC AAAGAGGCCT AAGAGAGATC AGTAAACCA CTGGNAAAGA AAAGATGGAG	60
AAAATGTTGG AAAACCAGAA CTGTNTGCTG TCAAGNTCAT GTGGAATGTT CAAGAAAGAA	120
TCTGACTCTA TTATCTAATA TCTTACATAC NTCCACCAGA CTGGACTTGC TATTTGAATT	180
TTAAGCAAGT TTCTTTTCT TTTATACAAA TTGCAAATTT CATATTTTAA TAATCACATC	240
CTAGGAATAG CACAATAATT GGGAAATAGA ACCCTTATCA CTAGNAGAAC CATTTTCCTG	300
CCACTCTCGA G	311

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

GAATTCGGCC AAAGAGGCCT ATGCCCCATA AAAGGGCTCC TGAAGCTCTT TGTGAAGGGG	60
TCTGAAAAGG GCAGATCAGG GTGTCCTTTG GGGCGGATGT GGGGTTTGGG ACAATTGCAT	120

GTGATTGTCA TTCTTTAGCT GTCTGCATCC CACAGAACT TTTTCTGAG TCTTCCAGCT	180
GGCCCAAGTC CTGGGTCTCT TTTACTGTTT TTGTAGCTGA CTACAGTAGG CAGATGAGGA	240
ACTCTTAGTC AATCTGGAAA AACTCGACTG ACTATAAACA ATCCTAAATT GAAAGAAAGG	300
TCTCGAG	307

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

GAATTCGGCC AAAGAGGCCT AGCCGGTGTG GGGAGGATTG GCTCAGCCAC CCGCTGGGAA	60
TCGTGCAGGG ATTCTTCGCC CAAAATGGAG TTAATCCTGA CTGGGAGAAG AAAGTAATTG	120
AGTATTTTAA GGAAAAGCTG AAGGAAAATA ATGCTCCTAA GTGGGTACCA TCACTGAACG	180
AAGTTCCCTC TCATTATTTG AAACCTAATA GTTTTGTGAA ATTCGTTGC ATGATTCAGG	240
ATATGTTTGA CCTGAGTTT TACATGGGAG TTTATGAAAC GGTTAACCAA AACACAAAAG	300
CACATGTTCT TCATTTTGGG AAATATAGAG ATGTAGCAGA GTGTGGGCCT CAACAAGAAC	360
TTGATTTAAA CTCTCCACGA AATACCACTT TGGAAAGACA GACTTCTAT TGTGTTCCGG	420
TGCCTGGGGA ATCTACGTGG GTAAAAGAAG CCTATGTTAA TGCAAACCAA GCTCGAG	477

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

GAATTCGGCC AAAGAGGCCT AAAAAATCT TCTGGAAATA ATTCTTAGCT GTGTAAGAAA	60
TTTGATACTT AAGGAGACAG CAGTGGAGTC ACTTAACTAA TTTGTGTGG TTTTGACCT	120
GCATAGTGAC TGCCATTAC TTTTATGTTT TGGTCAATTA GATACTAAGT AAAAAGATAG	180
TTGGTATTTT GGCTTCAGAT CAGGTCTATT TCTCCAACCT CTATATATCC TTTCTGTGAT	240
TAAACAAAT AAACAATCCT CAGTATCATC ATTTAACACC TCTAACTGAT AGAAAAAATG	300
AGGTTGTGGG TCCTCGAG	318

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GAATTCGGCC AAAGAGGCCT AACCTGGGA TTTTCTATAT ATATGATGGT CTCATTTGTG	60
NATAACACA ATTTTATTTT TTCCTTTCCA ATCTGGATGC TTTTTTTTTT TNCCTATTGC	120

ACTGCCTATT GCATTCCTAA AACTCCATT CCAATGTTCA ATAGAAATGG TGAAAGTGA 180
CATTGGAATG GAGTTTTTAG GAATGCACTC GAG 213

(2) INFORMATION FOR SEQ ID NO:292:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 644 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GAATTCGGCC AAAGAGGCCT AAAAAGAATT AACCAGCTCT TCAGTCAAGC AAATCCTCTA 60
 CTCACCATGC TTCCTCCTGC CATTCAATTC TATCTCCTTC CCCTTGCATG CATCCTAATG 120
 AAAAGCTGTT TGGCTTTTAA AAATGATGCC ACAGAAATCC TTTATTCAACA TGTGGTTAAA 180
 CCTGTTCCAG CACACCCCGAG CAGCAACAGN ACGTTGAATC AAGCCAGAAA TGGTTGCAGG 240
 CATTTCAGTA AACTGGGACT GGATCGGAAC ACTCGGGTTC AAGTGGGTTG CCGGGAANKG 300
 CGNTCCCACC AAATACATCT CTGATGGCCA GTGCACCAGC ATCAGCCNTA NGAAGGAGNT 360
 GGTGTGTGCT GCGGAGTGAC TTGCCCTGC CAGTGCTCCN TAATTGGNTT GGAGGAGGCT 420
 GTGGAACAAAN GTANTGGAGC AGGAGGAGCT CCCAGGNGTG GCGGTGTGTC AATGACAAAA 480
 CCNGTACCCA GAGAATCCAG NTGCAGTTCC AAGATGGCNG CACACGCACG TACAAAATCA 540
 CAGTAGTCGG TGCCNGCAAG TGCAAGAGGT ACACCCGGCA GCACANNAG TCCAGTCACG 600
 ANTTTGAGAG CATNTCACGT GCCAAGCCAG TCCAGCAACT CGAG 644

(2) INFORMATION FOR SEQ ID NO:293:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 299 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GAATTCGGCC AAAGAGGCCT ATTTNTGGAT GGTGCTAGCG AANTAGAGGC TAATCCCCAA 60
 CATGAGGTTT TTCTAATTTT ANGGTTGTGA TTTTCCAGTG AAAGAAATNA ANAAGAATTT 120
 GCAGATTCTG GGAGACTTGG GAAGGATATN AAGCTGTCTT ACAACCCCGAG ATTCACCCAA 180
 AATTCAGCAA ATCACTGAAT ATTCNNAATA AAAATTGAAG TATTTTCNAA CTCAGTTT 240
 TATCTCCAGA GGTNACGTC CNATGTAATC CGAAATCCTC ACGANGACAT AACCTCGAG 299

(2) INFORMATION FOR SEQ ID NO:294:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GAATTCGGCC AAAGAGGCCT ACAACAACAA CAAAAGAAGA ATACTAATTA GAATTTGAGT 60
 TCTAGGGGTT TTTCTAGGT TTTTCATTCT AGACTTAGCT TTTATTCAAA CCTGTTGATC 120

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CTGCATAGGG GTAGTCTAGC TTAAAAAAT AAAACAATAA ACATAAATGA GCCTATTGAG      180
TTCAATCAGA GTAGGGAGCA GTTTTATTGA ACAGCACATT TTCAAATCTC TCAGTTGTGT      240
TTTGTTTTTC AGCTACGTGT CTCTCTGTGA TAATGAAAAG ACAGGTTGCA AAGCCCGGGA      300
TTCGCTCGAG                                     310

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(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

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GAATTCGGCC AAAGAGGCCT ACATCTATTG AGGAAAACCA CAAAAAATT CAAAACAGCT      60
ACAACGGGAA AAAGAGAGTT TTGTCCACCA GTCAGCAGGC CACTAGTTTA TTAACCTCCA      120
GTCACCTTGA TTTTGTCTAA AATGAAGACT CTGCAGTCTA CACTTCTCCT GTTACTGCTT      180
GTGCCTCTGA TAAAGCCAGC ACCACCAACC CAGCAGGACT CACGCATTAT CTATGATTAT      240
GGAACAGATA ATTTTGAAGA ATCCATATTT AGCCAAGATT ATGAGGATAA ATACCTGGAT      300
GGAAAAAATA TTAAGGAAAA AGAACTGTG ATAATACCCA ATGAGCTCGA G               351

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(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

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GAATTCGGCC AAAGAGGCCT AGAGTGAGAC CTTATCTTAA AAAAAAAAAA AAAAAAATTG      60
TCTATGATTT TTTTAAAGC TTTTATTTT GAACATAATT TAGACTTGCT TAAAGTTGCT      120
AAAAATAAGA CACAAGTTTC ATATATCACT CAATCTGCTT CCTGTAATAT TAACAACATA      180
AATAGCCACA GGGAAATCTT CAAGACCTGG AAATTAACCT TAGGACAGCA CTATTACCTA      240
AACCACAGCT CTAATTTGAA TTTTCATCAGT TTTTCTCCTA ATGCTGATT TCTGTTCCAG      300
GATCCTATCC AGGAGCCAC ATTGCTCGAG                                     330

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(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

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GAATTCGGCC AAAGAGGCCT AAAAAAATAT AAGTAACAGA GGNAGAAATA ACTGTTATTTC      60
GTCAAGTGAC AAGCTTTTAA TGTCAGAATG GCTCACCTAA AGCGACTAGT AAAANTACAC      120
ATTAAAAGAC ATTACCATAA AAAGTTCTGG NAGCTTGGTG CAGTAATTTT TTTCTTTATA      180
ATAGTTTTGG TTTTAATGCA AAGAGAAGTA AGTGTTCAAT ATTCCAAAGA GGAATCAAGG      240

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ATGGAAAGGG ACATGAAAAA CCAAAACAAG ATGTTGGATT TAATGCTAGA AGCTGTAAAC	300
AATATTAAGG ATGCCATGCC AAAAATGCAA ATAGGAGNCA CCTGTCAGGC AAAACATTGA	360
TGCTGGTGAG AGACCTTGTT TGCAAGGATA TTATACAGCA GCAGAATTGA AGCCTGTCCT	420
TGACCGTCCA CGTCTCGAG	439

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GAATTCGGCC AAAGAGGCCT AATTATTTCT TGTCTCTCCC CAAATGAAAT CTGGGACATT	60
ATGACAATTT ATTTTCTAA GGATGATCTT GGTCTGCCT ATTGAAATGT CCTCACTCAC	120
CTCCAAGAGG AAGGGGGATG GCTTCAGAAA ATGTCTTTAA GTGTTTTTAT TTTTCACGAG	180
TTATTTATTG CAACACTAGC TCTTCCCTGC AGGAAGCTAT ATAATTGTGT GCTTAATTGG	240
TAACATAGAA GAATTCCTAG CTACTTCCTA GAGAATATAC TGTGAATTC CTTGTCCTC	300
AAGTATCTGT TAAAACTCA ACCGTGGGAA ACAATGTCTA TGGATGCCTT TGGGAAAATA	360
CACATTTTAC CTATTATTTT ATCTTTTTC TCACTTTGTC AAGTAGTAGG TACCCCACTG	420
TACTCGAG	428

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GAATTCGGCC AAAGAGGCCT AACATTATCG ATTCCATTTT TTTACTGTTG TAATTCTGCT	60
TCTTATTGCC TGTGTAAATT TCTGCTCTAT ATTAGTTTCC TGATACCCCTA TCATTAATTC	120
AGTCTGCCCT TTTTCATAT CATTCTACTG TTTGTCTCA TCTTCCTTAT ACTTTATTCA	180
GAGACTGTGT TTTTCATGAAG TTTGTGAAAA ACATTTTAAA AATTGTTTAA AATGTACTCT	240
TTGTCTATTT CTTGCTATTT TTTCTTTTGT ATATTCTGGA ATATATCCAC AGCGCTCGAG	300

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GAATTCGGCC AAAGAGGCCT ATAGATTGTT ACATTTGTTT TGTGCATTCC ATGAAGTTTC	60
TTACCCTTAG AGTTATTTCT GTCTTAGTAA CAGCAACAAG TGGGAATGGA GACTTTGGTG	120
ACTGGAGTGC CTTCAACCAA GCCCCATCAG GCCCTGTTGC TTCCAGTGGC GAGTTCCTTG	180

GCAGTGCCTC ACAGCCAGCG GTAGAACTTG TTAGTGGCTC ACAATCAGCT CTAGGCCCCAC	240
CTCCTGCTGC CTCAAATTCT TCAGACCTGT TTGATCTTAT GGGCTCGTCC CAGGCAACCA	300
TGACACTCGA G	311

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GAATTCGGCC AAAGAGGCCT AGCGCGGTGT GTCGTGGTGT GGCGCGGTGT GGCATGGCGT	60
GGTGTCCTCCAG CTGCTACAC ATTTGTGGTT TTTAAATGTT TGTGGATAC AGTAACACTT	120
TGTTAATTTT AATTATATGC AAGATAACTT GATTGCCCTA AAACAGCCAT TTGGGTCAAG	180
ATAAAGCCAT CGCCCTCTGA AGGGGNTGA GCTGGGTGTC TCCTCCATCA GTCGNTGTGA	240
TAACTCTATG CCAGTTTCGA TTTCCAAAGT CAGAAGTGCA AAGCAGGGCT GGTATTATAT	300
CNTGTCAAAT CGTCCAGGTC CTGTGTNGTC GNACTCCATT ANTTATNTAG GTCCATANGA	360
TGTGTCTTAC NACGNAACAA ACCCTCTCG AG	392

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GAATTCGGCC TTCATGGCCT AATGGAATTT GAGTCCAAAG GTAAATATAT TAAACATATA	60
GATAAGAAGA AAAGAAAAAC GTTATTTAAG TATCTGATCA GCTCTGCACC CCAGGGACCT	120
CCACTTTTGC CCAGGTTTGA GAATTTGATC TATAGAATTA CCTGCATTCT TTCCCGCTCA	180
TCCATCCAAT CAGCCACCTT TCTCCCTTCA AAGAAGTGTC TTCATTTTTT TCCTTCTTTT	240
GTTATTTTTA TTGACTGCCC ATCACTGTTA TTAAATCCTT CCCTCTTTTT TTGAATGAAG	300
CAGCAGAGCC TTTTATTTTG TTTTCCTTGT TTGTTTTTTT GTTTTTGTGT TTCAGAAATG	360
ACAGGGCTGT ATCACAGCAG TCTCGAG	387

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GAATTCGGCC TTCATGGCCT AAAAATTAAG CAAGCAATAC CTAGCCAATA GTTCTGCTTA	60
ACTTTTNGGT TAAGTATTTT GTTGGGATTC CTATAAATAA TTTTTCACAC AAAGTTTAA	120
ATTCTCGGTG TACTTTGACT CTCAACTGAG AGTGGATAGA GTTTTTCTTT TGAGGATTAC	180

ATCTTAAAAAT GTCCATCGCC TGGCTGGTTA TAAGCATTTG TCACCTTTTG AAGGTAAAAAT	240
ATACTCTGGC CCTTCTTGAC TCAGTTACAG GTCATTTTAG GTCCAGTAAT AAGAGTCAGG	300
TGTTTGGTTA TTGCTTTCAG AGTCAGACAA ATCTCGAG	338

(2) INFORMATION FOR SEQ ID NO:304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 478 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAATTCGGCC TTCATGGCCT ACGAAGAAAA AATATTTTNG AGAGAATTTC CCAGATTGAA	60
AGAAGATCTG AAAGGGAACA TTGACAAGCT CCGTGCCCTC GCAGACGATA TTGACAAAAC	120
CCACAAGAAA TTCACCAAGG CTAACATGGT GGCCACCTCT ACTGCTGTCA TCTCTGGAGT	180
GATGAGCCTC CTGGGTTTAG CCCTTGCCCC AGCAACAGGA GGAGGAAGCC TGCTGCTCTC	240
CACCGCTGGT CAAGGTTTGG CAACAGCAGC TGGGGTCACC AGCATCGTGA GTGGTACGTT	300
GGAACGCTCC AAAAATAAAG AAGCCCCAAGC ACGGGCGGAA GACATACTGC CCACNTACGA	360
CCAAGAGGAC AGGGAGGATG AGGAAGAGAA GGCAGACTAT GTCACAGCTG CTGGAAGAT	420
TATCTATAAT CTTAGAAACA CTTGAAGTA TGCCAAGAAA AACGTCCGTG CTCTCGAG	478

(2) INFORMATION FOR SEQ ID NO:305:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 568 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GAATTCGGCC TTCATGGCCT AGACGAGCGG AGTAAATCT CCACAAGCTG GGAACAAACC	60
TAGTCCCAAC TCCCACCCAC CGGCGTTTCT CCAGCTCGAT CTGGAGGCTG CTTGCCCAGT	120
GTGGGACGCA GCTGACGCCC GCTTATTAGC TCTCGCTGCG TCGCCCCGGC TCAGAAGCTC	180
CGTGGCGGCG GCGACCGTGA CGAGAAGCCC ACGGCCAGCT CAGTTCTCTT CTACTTTGGG	240
AGAGAGAGAA AGTCAGATGC CCCTTTTAAA CTCCTCTTC AAAACTCATC TCCTGGGTGA	300
CTGAGTTAAT AGAGTGGATA CAACCTTGCT GAAGNTGAAG AATATACAAT ATTGAGGNTA	360
TTTTTTTCTT TTTTTTTTCA AGTCTTGATT TGTGGCTTAC CTCAAGTTAC CATTTTTTCA	420
TCAAGTCTGT TTGTTTGCTT CTTAGAAAT GTTTTTTACA ATCTCAAGAA AAAATATNTC	480
CCAGAAATTG AGTTTACTGT TGCTTGATT TGGACTCATT TGGGGATTGA TGTTACTGCA	540
CTATACTTTT CAACAACCAA GACTCGAG	568

(2) INFORMATION FOR SEQ ID NO:306:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GAATTCGGCC TTCATGGCCT AATCAAAAAT ACCTTACCTT GTTCTGCCCT GTGAAAGTAG	60
CCTAAGGCCT GTCAAAAACA CAAAGAGCCC AACATAATA AAAAAGATTA AAGAAGACAA	120
TATTAAANAA GCATTGTCTC AAAGATCTAC TGCTATATTA TATTTAAGTC AGGAAGTAAA	180
TCATCTTAAA ATAATGGTCA CTTCTTCAAC AGTGAGAGTT AACACCCAAA GTGAACGTAA	240
CACCTTCAATC ATCAAGATTA CAATATATGG ACTACTTCTG GTAATAACTT GGTGTGTT	300
TAGAACTTGT ACCAAACTAA CATCATGTGC AGAGAGGAAA GAACTCGAG	349

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GAATTCGGCC TTCATGGCCT AGTGATGGGG ATGTGATGTG GGCATCTGCT AATTCGTCTG	60
CAACTACATG ACCTAAGATG GCCTCATTA TCTAAGGGGC CTCAGCTGGA ACACTTGCCT	120
CTGCTGGATA ACCCAGGTCT AGTGTTATCC TCCAGACTAG ACCTGGCTTC TTCTGTGGCA	180
GTCTCAGGGC AGTGTTCCTA GACGGTGAGA GCAGAAGCCT AGGTTTGGCC ACATATCCCT	240
AACTCATAGG ATGGTGACAT AAACCTCTACC TCTTATGGAG AAATAGCAAG TTACTGCA	300
TACGGGACGA CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAATTCGGCC TTCATGGCCT AGTGGCAACG ACTTGGACAT CTGAGCTGTC ACTGCCGAAA	60
ACAGGCCGCA AGAGAGATAA TCAATATGCA TTCCAAGCC TTTTGGCTAT GTTTGGGTCT	120
TCTGTTTCATC TCAATTAATC CAGAATTTAT GGATGATGAT GTTGAGACGG AAGACTTTGA	180
AGAAAATTCA GAAGAAATTG ATGTTAATGA AAGTGAACCT TCCTCAGAGA TTAATATAA	240
GACACCTCAA CCTATAGGAG AAGTATATTT TGCAGAACT TTTGATAGTG GAAGGTGGC	300
TGGATGGGTC TTATCAAAAG CAAAGAAAGA TGACATGGAT GAGGAAATTT CAATATACGA	360
TGGAAGATGG GAAATTGAAG AGTTGAAAGA AAACCAGGTA CCTGGTGACA GAGGACTGGT	420
ATTAAATCT AGAACAAAAC TCGAG	445

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

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GAATTCGGCC TTCATGGCCT AGAAGTTCCT TATGCTACTT TCACTGAGCA TCCTATGAAA      60
TACACCAAGTG AGAAATTCCT TGAAATTTGC AAGTTGTCTG GGTTCATGTC TAAGCTTGTT      120
CCAGCTATCC AGAATGCCCA CAAGAATTCA ACTGGATCTG GAAGAGGAAA GAAACTGATG      180
GTGTTAACTG AACCCATTTT GATTGAGACC TACACAGGGC TGATGTCATT CATTGGAAAC      240
CGCAACAAAC TTGGCTATTC CCTTGCCCGT GGGAGTATTG GTTTTTGAGA GTC'TTTTGG      300
TACCATAAGC ATATCATCCA CAGATATGTC ACTTTGAAAA TTCCAGTTTG ACCCAGGCTA      360
TTTTTGGAAT NAAACAATTA ATTATTTTAA AATGACGCTT TATGATTTAG AAATTAGTA      420
TTCCGAAAAA TTTAAAAGCT TGATTGGACT GATAGATACA CACTTTAGAC CTCATACAAG      480
AATAATCAAA TTTTCTTAAA ACTAGAAAAT AAATGCTGCT GATACCTCGA G              531

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(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

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GAATTCGGCC TTCATGGCCT AACTCATGC TGCCAGTCCC CAAAAGACTT CATTTCATCA      60
ACATATATGT GACCGCCTGC TACGTGCCAG GCGTGGGCCA GGTCCTAGGG ACAAAGGAGA      120
GGCCTCCGCA CCCCACCCCA TGACCCATAC CTCCTCTTCC CCACCTCCCT GGGCCAGCCT      180
GCCTTCCTTC TCCCTCCTCC TCCTTCCTGG GGAAGGAAG CCCCACCTTC TGTGCGCAGT      240
CAGCTCCTAA GCACGCTCCC GCTTCCCTG GCTCCCCAT TTAAAAAGGG AGGCAAAGGA      300
TGTCACCACT GTCACACAC TCATGGCTTT GCTCTGGGAA GTCCTGCAAA TAAATGAAA      360
GTTCTCCAAC CCGTACTCGA G              381

```

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

```

GAATTCGGCT TCATGGCCTA CTTTGACGCA CCAGGCACAA CCCAGAAAGA CGAGATTGTG      60
GAAATCCATG AGGAGAATGA GGTGCGATCT GGTACCCAGT CAGGGGGCAC AGAAGCAGAC      120
GCAGTTCCTG CACAGAAAGA GAGGCCTCCA GCACCTTCCA GTTTTGTGTT CCAGGAAGAA      180
ACTAAAGAAC AATCAAAGAT GGAAGACACT CTAGAGCATA CAGATTAGA GGTGTCAGTG      240
GAAACTGTAT CCATTCTGTC AAAGACTGAG GGGACTCAAG AGGCTGACCA GTATGCTGAT      300
GAGAAAACCA AAGACGTACC ATTTTTCGAG GGGCTCGAG              339

```

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

GCCTGCCTCG	AGTCTTGGAT	ACATCACACT	TGAGTCAAAT	CCTGGATACT	GCCAAAGGAA	60
CCTGAAAATC	CAGGAGACAA	CGCTAGCTAT	TCCTGTGAAC	CTCTAGAGGA	TTTGCGCCTG	120
CTCTTCAAAC	AACAACCAGG	AGGAAAGTAA	CTAAAATCAT	AAATCCCCAT	GGCCCTCCCT	180
TATCATATTT	TTCTCTTTAC	TGTTCTTTTA	CCCTCTTTCA	CTCTCACTGC	ACCCCTCCA	240
TGCCGCTGTA	TGACCAGTAG	CTCCCTTAC	CAAGAGTTTC	TATGGAGAAT	GCAGCGTCCC	300
GGAAATATTG	ATGCCCCATC	GTATAGGAGT	CTTTCTAAGG	GAACCCCCAC	CTTCACTGCC	360
CACACCCATA	TGCCCACACT	CGAG				384

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GAATTCGGCC	TCATGGCCT	AGGGGGTGG	GCTGATGGAG	GGTAAGTAAA	ACCTCCTACT	60
GGAAGATGTT	CTCCTAAGAG	TTCCACTTCA	TTTTCTATCC	TTTGCAGAGG	CGATCGTGAT	120
TGCTGTGTTT	GGAAGGGGAC	AACTGGCCT	GGTGGTGGCA	AATGAGGAGG	ATGATGGGGA	180
GAAAGGTGAG	GAGGATGTAT	AAGAAATGGA	TCACTAGAAA	TAAGGGGTGG	GAATGCAGCA	240
TATGGTACTG	GTAAGTGCTG	AACTGAACAT	GCCTGAAGCA	TTGGAGGAGG	CACACTACAG	300
ACAGGGAGGT	GCTGTCCACT	AAAACCACA	GAGCATCCTG	GGACCTGCTG	TGTACTACAA	360
GCAGGGATGT	GCTGGCCTGT	GCAGAGTGGA	ATCCCATGTG	GTGCCACTGT	TGTTACTGTG	420
TAAGAAACAG	GGACTGTTCC	TTGATGGAGC	TGATCATGTA	TGTCAACCAT	GACTGCATTG	480
TGCTGGGGTG	GATGAGCAGC	AGGATGTAGC	AGACGGGGAG	ATACATTCGG	AGGGTGGGAG	540
GCTCGAG						547

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GAATTCGGCC	TCATGGCCT	AATTTGTGGC	TTACCTCAAG	TTACCATTTT	TCAGTCAAGT	60
CTGTTTGTTC	GCTTCTTCAG	AAATGTTTTT	TACAATCTCA	AGAAAAATA	TGTCCCAGAA	120
ATTGAGTTTA	CTGTTGCTTG	TATTTGGACT	CATTGGGGA	TTGATGTTAC	TGCACTATAC	180
TTTTCAACAA	CCAAGACATC	AAAGCAGTGT	CAAGTTACGT	GTGCAAATAC	TAGACTTAAG	240
CAAAAGATAT	GTTAAAGCTC	TAGCAGAGGA	AAATAAGAAC	ACAGTGGATG	TCGAGAACGG	300
TGCTTCTATG	GCAGGATATG	CGGATCTGAA	AAGAACAATT	GCTGTCCTTC	TGGATGACAT	360
TTTGCAACGA	TTGGTGAAGC	TGGAGAACAA	AGTTGACTAT	ATTGTTGTGA	ATGGCTCAGC	420
AGCCAACACC	ACCAATGGTA	CTAGTGGGAA	TTTGGTGCCA	GTAACCACAA	ATAAAAGAAC	480
CACACTCGAG						490

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GAATTCGGCC	AAAGAGGCCT	AGGAAGTAAC	AGTGTATCAT	GTATGCCACT	GATTCCAGGG	60
GACACTCCCC	TGCTTTCTC	CAACCTCAGA	ATGGAAATAG	TCGTCACCCA	TCTGGCTATG	120
TTCCAGGGAA	GGTTGTCCA	TTGCGTCCCC	CTCCTCCTCC	AAAGAGTCAA	GCTTCAGCCA	180
AATTTACCTC	CATCAGACGA	GAAGACCGGG	CAACCTTCGC	ATTCTCACCT	GAAGAACAGC	240
AAGCCCAGAG	AGAAAGTCAA	AAGCAAAAGA	GACACAAAAA	TACTTTTCATT	TGTTTTGCTA	300
TTACTAGTTT	CTCATTTTTT	ATAGCACTTG	CAATCATTTT	AGGAATATCC	TCAAAATATG	360
CTCCACTCGA	G					371

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GAATTCGGCC	TTCATGGCCT	AATTTAAATG	TGGACAGATT	GGAGGGGAAA	GGTTTGCAGC	60
AAAAATCATA	AGTAGAAGGA	AACAGAATGG	TTAAGTACAC	AGTGTAAGTAG	CCATTTAGGA	120
AAGTTATAAG	CCATTTAAAT	GCCATGTATA	AAGTGTTTTT	GATAAGAAAA	AATCAAAGTG	180
TAAAGGAGAA	TACAAAATTA	TATGTGTACT	GCGGACACAT	CTGTATTGTT	CTGTGTATGG	240
AAAACAGACT	GGGGAGAAAT	AGCTTTAAGT	CCTAATAGTA	ATTTCTTTT	TCTCTCTTCT	300
TTTTTCTGCT	TTCTCTTTTC	CCTGTCTCCC	TCAATATTGC	ATATCTTTCC	CATTAAAAAG	360
TATTGTATTA	TATATCTACC	AACAAGACAT	TTGTTTCAGA	TTTTTTGGTT	TTGTCTTCAA	420
GGAACATTCT	TCTGCATACA	AACCTGAG				448

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

GAATTCGGCC	TTCATGGCCT	AGAGATGGGG	TTTTGCCACG	TTGCCCAGGC	TCATCTCCTC	60
GAACTCTTGG	ACTTAAATGA	TCCTCCCGTC	TTGGCCTCCG	AAAGTGCTGG	GATTACAGGC	120
ATGAGCCACA	GTGCCCAGCC	TCTACCCGCT	TTCTGTGGTC	AGAAATAGAC	GCAGGACATT	180
CCATCCATAC	CTTATTCTT	TCCTGGCTCT	TCTCCCATGT	GTCCTCGTGG	GTCCTGGTCA	240
CCCTCTTAGC	TGCTGTGTAA	TAACCCCTGT	GCAGATGCAG	CAGCCACGAT	GTCATCAGTC	300
CCCACCCAGT	GATGCATAGG	GGGCTTCTTC	CCCTCCCTGG	GTACAGCACT	ACCAATTCCT	360
GTGTATGGGC	CGTGTCAAGC	AGGGGCCACG	TCCTGGCCCC	GCTTCAGTCC	CGGCTCGGGC	420
TCCTCGCCGG	GGTCTCCATG	CCACTTCCCT	CTCCCATCTC	CACATCTCGA	G	471

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

```
GAATTCGCCT TCATGGCCTA CAGCATCGTC GGGACCAGAC TCGTCTCAGG CCAGTTGCAG      60
CCTTCTCAGC CAAACGCCGA CCAAGGAAAA CTCACTACCA TGAGAATTGC AGTGATTGTC      120
TTTGCCTCC TAGGCATCAC CTGTGCCATA CCAGTTAAAC AGCTGATTCT GGAAGTTCTG      180
AGGAAAAGCA GCTTTACAAC AAATACCCAG ATGCTGTGGC CACATGGCTA AACCCTGACC      240
CATCTCAGAA GCAGAATCTC CTAGCCCCNC AGAATGCTGT GTCCTCTGAA GAAACCAATG      300
ACTTTAAACA AGAGACCCTT CCAAGTAAGT CCAACGAAAG CCATGACCAC ATGGATGATA      360
TGGATGATGA AGATGATGAC GACCATGTGG ACAGCCAGGA CTCCATTGAC TCGAACGACT      420
CTGATGATGT AGATGACACT GATGATTCTC ACCAGTCTGA AGAGTCTCAC CATTCTGATG      480
AATCTGATGA ACTGGTCTCG CTCGAG                                         506
```

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

```
GAATTCGGCC TTCATAATTT TTCTTATCTT CATTCTTTTC GGTGCCCAA TAAGCTCATG      60
TTTTCCATGG TCGGTTTAGT TTTTACTAGT CGTTGGCTAG TTTCTAATT GCATGTGAGT      120
TAGCATGTGG TGATGGCGGA GTAATGTCAT GTCTGGAGA GAACATTGCT TGAGTTCCAA      180
ACTTAGCTTT TCTACTTCTT GGTGAGACTT TGGACAAATT ATTTTGGAGC TTGTTTCCTC      240
ACTTAAAAAA ATGGGGTTTG TACCTTTAGT TGTTTCAACT GTTGTGAGGA CTTGAATAAT      300
AAAGTATATA GCTATAGATA AGAAAACCTG GGGGACTCGA G                                         341
```

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

```
GAATTCGGCC TTCATGGCCT AATTTTTC AAAACCTTGA AATGACATGT TAAAATGCTG      60
CTTTGAACTG GTTTTCTTT AGCCTGTAGA AAAGAACCTT GAGTTACTGG TCAAGTAGTT      120
TTGACCATAC TGGCTTAGGA AAACAGCGCA TCAGCTGTCT GATTGCTATC ATGTAAAAAT      180
CTGTGAACGA CTTTGAGAAG TCATTGGTGG ATTATGTTGT TCAGGAATAG GAATGGAGCT      240
TTCTTCCTAT CACTTGATTT TTTTTCCTT TTTGGAAGGG GGGAGGAGGA GGAATTATTT      300
CCNCCCTAAT AAANGGNGGN NTTAATCCTG GGCCCCNNA AGGCTGGNNN GGGTCCNGAT      360
KTGGGGGTNC NNTTTATTGG GAACTGACNG GGNTTTAATT TTCCGGTTTT TTTTTCCT      420
TGAATGATCT TGTGTGTAG AGTTGAATAC AGTTCTAGGG AAGTATGATC ACAAATGAA      480
TGTGGCAGT TCCTCCTATG ATTAATATGT CAGACATGTC AAAATTCTCT CATCATGTGT      540
```


ATTGCGGG TTTATTCAGT CCAGGACTCG AG

572

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```

GAATTCGGCC TTCATGGCCT AGATAACTTT GAACAGAATG GGAGGCAGGT TTACCCTAAG      60
CAGTTCCTCCA CTGAAGTTT TCCTTTAGTT TAGTGATTG AGGGGCCCAA AATACTTTCA      120
CATTTCCCCC CTTTCTTTT TAAAAATCTG TTGGAGAACG CATTTTAGAA GAAAATGAGT      180
CTCTGGCCTC AGGTTTCGTC TGATCTCTCA TGGCTAGGAT GGTTTATTCC TAGATAGATA      240
GGTCCTGAGT TATTAGGAAA GTCCTTTTTT AGAAGGTGT GAAGTCTCAT GTCCTGTGAA      300
GAGAAAATAG GGGGAGGACA ACAACAAACA AAAGAACTCG AG                        342

```

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

```

GAATTCGGCC TTCATGCCTA CAATATGTT TAATAATTAT TCAGAAATAT TCAAGTATAA      60
TACTTAATAA AAATTCTGCT TATGTGCAAG GCATGGTGCT AGGTACTGAG ACTATAAGGA      120
GGTAAAAGAT AGTTCCTGCC CTAAAGACT TCTATAATT AATCAGAAAG GAGAGTATAT      180
GAAAATCATA CTGAATAAAA AGTGGCTCAT AATAAATGCC AAGGAATCAA CACAAAGTCC      240
TTCCCTGGT AGGGAAAGTT TTTTGAGGA AATGGGACAT GAATTGGCT TTGAAGGATG      300
TGGAGGTTT AGATAAGAGG GAGAACTGT TGTGTTCTAG GTTAGAGGAA CAACATAAAC      360
TCAAAGAGA CTAAGAAGA ACGGACTCGA G                        391

```

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

```

GAATTCGGCC TTCATGGCCT ACCCTGAGCA GTGCCTGGCC CATACTGGAT ACACAGTGTG      60
CATTTTGTGG GGAATCAAGG AAGGAAGGTA ATATCCAGC TCAGGGTTCT CTCTGACCCT      120
GAATAGTGTT ATGGACTCTT TGGGAAGGAT AGAAGCTTTC TTAGTTTTCT GACAGAGGCC      180
TGTAAGCTGC AAACGTTGTG TTTGTAGAAA GAGTTGTAAA GGTGTCATGA GCCTTTATTT      240
AAAAGTGTCT TTAATGTATC TTAGGCATCT TTTCTTTTC ATCTCACACT ATGGACAGTT      300
TTAAGTGCAA AAGGGGAACG CGAG                        324

```

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

```

GAATTCGAGC TCGACTGGAT AGTTTTTCTT TTTAACTTA AAATGCTTT TAGTTTGGCA    60
CTCCGTAGTA AAGGAGGTTC CAGAAGCCAG TAAGAGAACC TCTGCCAACT ATGAAAGAGA    120
AGATATTTCT ATCTACAAGT TATTTTCAGGA TCAATTATTC AATTAATATT TTATATAATA    180
GAAAGGTTTT ATTTGTTAGG ACTTTATCTT TAAGTTCCTT AAGAGTAAAA AGGTCTAGTC    240
ATTATTATAC TGTGGGAGAA TGATAGAAGA TTGATTACAT TGAAGTCCA GAACCTCTAT    300
TTATTAAAAA GATTTAAGAT TTGACACACT CTCGAG                                336

```

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

```

GAATTCGGCC GGCATGGCCT AANCTAAAAA TAAATNAAC CCAACGCATA NAANACGGGT    60
TTATCTCTCC TAAAAACANT TNAGTTTNGA CTAAATGAA ACANATCATN NNACAACTC    120
ATTTTNAAT GAAGATTTTA CCTGGACCCT AGGTGTGCTA TTCTTCCTAC TAGTGGACAC    180
TGGACATTGC AGAGGTGGAC AATTCAAAAT GAAAAAATA AACCAGAGNA GATACNNCG    240
TGCCACAGAT GGTAAAGAGG AAGCAAAGAA ATGTGCATAC ACATTCCTGG TACCTGAACA    300
AAGNATAACA GGGCCAATCT GTGTCAACAC CAAGGGGCTA GATGCAAGTA CCATTAAAGA    360
CATGATCACC AGGATGGACC TTGAAAACCN GNAGGAAGTG CATCTCGAG                                409

```

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

GAATTCGGCC TTCATGGCCT AGGCGGCGGC AGCCGAGGGC GTACTGGCGA CCCGGAGTGA    60
TGAGCCCGCC CGAGACGATG CCGCCGTGGA GACAGCTGAG GAAGCAAAGG AGCCTGTGTA    120
AGCTGACTTC ACTGAGCTCT GCCGGGACAT GTTCTCCAAA ATGGCCACTT ACCTGACTGG    180
GGAAGTGACG GCCACCAAGT AAGACTATAA GCTCCTGGAA AATATGAATA AACTCACCAG    240
CTTGAAGTAT CTTGAAATGA AAGATATTGC TATAAACATT AGTAGGAAC TAAAGGACTT    300
AAACCAGAAA TATGCTGGAC TGCAAGCTTA TTTGGATCAG ATCAATGTCA TTGAAGAGCA    360
GGTAGCAGTT TTTGAGCAGG CAGCTTACAA GTTGGATGCA TATTCAAAAA AACTGGAANC    420
CAAGTACAAG AAGCTGGAGA AGCGATGAGA AACTTATTTC TATGGGACAG AGTCTTTTTT    480

```

TTTTAATGTG GAAGGACTCG AG

502

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GAATTCGGCC TTCATGGCCT AGAATATTCC ATATCAGTAC ATATAGCACT GCCTCACTTT	60
TTAATGGCTA TATAAAATAG TACTATAATT TTAAACCACT CACCTGATGG TGGGCTTAGT	120
AGTTATTCTG TGGCTGTAAC CAACATCACT GCCATGTGCA CTGGTACACA TACAGAAGTC	180
CACACAAGTA GGCCTGTATC TGTAAAGTAA ATACTGGTGG GATTACTGAG TGAAAGGAGA	240
CGTGAATTTT TAGATTTTTA CTATGAAAGA CAACTGCTC TTTATGGGGA TTTTATTAAT	300
CTACAACCCC ATCAACAATG TATGAGAGCC CATTTTTCAC ACACTTGCCA ACTCAGTAGG	360
TTATTAAACC TTTTGGTCTC TGCCACTTGT ATATCCCAGA TCAACTTCTA ATTCTGCTTC	420
ATATTGTTG CTATCCTTTA GAATATTTCT GTCCCACCTT GTCTCGAG	468

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GAATTCGGCC TTCATGGCCT AGGGAAAGGA AGTGACATAG TGGTATAAAA ATTTGAAATT	60
TGTGATGTGG CTTAGAAGCT TGATATATAC GGGTATGATT GCAGCTGCTA CATTTAGCCT	120
TTTTTTCTTT CTTTTTGGAG AATGAACCGC ATTAAGAAAT ACATTTTACA TCACAATTTA	180
GCAAGTATAT GTGCTAACAT ACTTCTGTTT CTACAAGGGA TGTATTGTGG TATTTTCTAT	240
TGCATTTTAC TCTAATTTAG TTCATTTAAA AAAATGCTGA TTCTAACCCA TGAAGTCGAG	300

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAATTCGGCC TTCATGGCCT ACCACCACAC CCGGCTAATT TTTTGTATTT TTAGTAGAGA	60
CGGGATTTC A CATGTTAGC CAGGATGGTC TTGATCTCCT GACCTCGTGA TCCACCCGCC	120
TCGGCCCCC AAAGTGCTGG GATTACAGGC ATGAGCCACC GTGCCTAGCC GACTCTTGAG	180
TTTTGACAAG AGGTGATATC TGGGAGATTA ATAAGTATTT AGTTTAAGAA AACATTTAGT	240
AAGCCTGTCC TGTGTTCCCA CACAAAGGGT ATAACAGCAA TATATTCCAT AAGAGTAAAG	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

```

GAATTCGGCC TTCATGGCCT ACATTACCAT CAGATTGACA TATTTAATTA TCAGATATCT      60
TTCTTTTGCC AAAAAGTTGT GGTGAGTTG GCCCTGGGAT TTATAAATAC ATGCACACAG      120
CACATTTCTG TCATTGTTCA CTGCAGTCTT TTAACACATC TTCTCAGCAA TATTCTTAAT      180
GTTTCACGCG GGAAAATTGT AAATTATTTA ACCACTGAAT TAGAGGTGTG TTGTTTTTTA      240
GCTAATCAAT AGCCATTGAA TGCTTAAATG GGCTTTAAAG TAGACAAAAG TAAAAGACAG      300
CAAAGAAAAT TAATCAGTAA GATTGCCCAT ACTCCATAGA CACTTGAGCA GCTACTTTAG      360
TCATTTTGAA ATACACGCTT TATGTTTCC CTTGGACTGG CATATTCCTG TCATTTATAA      420
AAAGAATATA CATTGTGAAA TTTAAGGTGT GGACATTCAT TATTGAAGGT AGAAATAGTT      480
ATAATCATCA GTGTCTAGAT ATATCTGAAG AGAGGTACTC GAG                          523

```

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

GAATTCGGCC TTCATGGCCT AAAGTAGGCA AGGGATAATA ACCAAAGAAG NAAATTTTCAT      60
GAAGACTAGA CATCATAAAG CATAATTTTA ATAGTCACTC AACCAAGTAT TTTTATTTT      120
TTATGGATAC TCTGAATGGC AATTAAATGT GAAACCCAGT TTCTTGGGCA AGTCAAATTC      180
TGGAATCACA TCCACCTAAA TTAAATGAC TAGCTCGTAT TTTCCCCATC TTCAAGTTTC      240
ACATCCTGGT CATCAAAGA CTCGACAGCA AGACTTAGAA TGAAAAAGGG TACTTGTTTA      300
TATTAATATT TTTTACTTGA ACACGTGTAG CTTGCAGCAG GTTCTTGATG AATGTGCTTT      360
GTGTCCAAAA TGCCTCCCA TTGTACACAG GTGTACACCA TGCATGCACC AACACCCTC      420
GAG                                          423

```

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

```

GAATTCGGCC TTCATGGCCT ACAAGCCACA AAAGTGTGGT GAATGGAAAA GAATGTATAA      60
ACTTCGCCTC ATTAAATTTT CTTGGATTGT TGGATAACCC TAGGGTTAAG GCAGCAGCTT      120
TAGCATCTCT AAAGAAGTAT GGCCTGGGGA CTTGTGGACC CAGAGGATT TATGGCACAT      180
TTGATGTTCA TTTGGATTG GAAGACCGCC TGGCAAAATT TATGAAGACA GAAGAAGCCA      240

```

TTATATACTC ATATGGATTT GCCACCATAG CCAGTGCTAT TCCTGCTTAC TCTAAAAGAG	300
GGGACATTGT TTTTGTAGAT AGAGCTGCCT GCTTTGCTAT TCAGAAAGGA TTACAGGCAT	360
CCCGTAGTGA CATTAACTTA TTAAAGCATA ATGACATGGC TGACCTCGAG	410

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

GAATTCGGCC TTCATGGNCT ACCTTAGCCT CAGCTCTTTC TTCTGGGTTG TTGTATTTT	60
CTTTTCTGTC CCAAACAGTT TCCCCACAA AAAGAACTTT ATGTCTTTCT CTGTCTTCCC	120
TCAGTCCTTC CAGTCAGCAG CCTGTGATTG GGCTTTTCCC CTCAGAAACG AACAATCCAG	180
AACCCACTGT TAAAACAAC TGTATTTTGC CTTGGGAAGT CCCATTGCCT TCCCTGAAAA	240
CATTAAACAT TCCTCCGATC CCCAGCCTGA GTCTCTCTGT CTCTGGGCCC CATCCTGCTC	300
CACAGCAGGG CTGGTGTGTC CAGCACAGAG TGACCTCCG ATGCCCTTTC CCACCCGCCG	360
CCNTGCCTCC CTCGAG	376

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GAATTCGGCC TTCATGGCCT ACGGGTTGTT ACATATTTAT TCTTTTTTGA AGCCCATCAC	60
TACATCGCCA TTACGTTTTA CACTGTGTAT GTAACAAATG TTACCACTTT GTTCTTTATT	120
CCTTTTTTGA TCATCTTCAG TGGGGGTAAA ACAGTATCAA GCTCTAGAGC TCCCTCTGGT	180
GGTTTTTGTG ACATATTTGA AGATGGCAGC TTGCTTTTGT AGAATTTCTG GCTCTGCTCT	240
CCCTGTTTTT ATCTGTACTT TTTTCTCTCA TTGTGCCTCT TGCACACACA CACCCCCCCC	300
ACTCGAG	307

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCGGCC TTCATGGCCT ACATTACTCA GCTTTCCTGA ACAACCAGGC ACGACCCTCT	60
GCCTGCAGGC CAGGCACGTG CTGCTGCCCC TGGAGGCGGG TGGGGGTGCC TCCGCGCTGG	120
AGGACACGGG GTGCACTGAG GCTTCCCATG GGTGATGGGG GAATGTGGTG ATGAGGGGAT	180
GCGGTGCCCG CGGACCGCAC ACATGCCATG TGTGGACACT CAACAGGAAG CTTCGGTCAG	240

CATTTCAGCT GGAAATGCAG AGCCAGGGCC CTGGAAAGTC CCTCAGCAGC TGTGCACAGG	300
CCTGCTCACC GTGCGTGTGC GGCAGAGGCC TCCCTGGGGA GGCAGAGGCC CCGCGTTCTG	360
CACTCGAG	368

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GAATTCGGCC TTCATGGCCT AATTGAATTC TAGACCTGCC TTCCTGCTCT TCTAGGTAGT	60
CACACTTCAC TAAAGTGTCA TCCACCACTG TGTGAATCC GAAGAATGAC AATTTTCTAC	120
CACTGGTGTG AAAAACAAAC ATTTGAAGAC CCTTGTGCAT TGTGTGTCAC AAAGCTAAAT	180
ACATGGAAAT CGTTAATATC GCTGATATTA AGTAATTTCC CCACTCTGAG TGAATACTTT	240
GATGATTGCC AACAGTGGCT AATAAAATGA CGGCTACCAC ACTCATGGGT CACTGGGGCT	300
GCGCAGGGCT CTTTGAGGTG GGTGGCTTCT TTTGGAAAGT ACTATGAACG TCTCGAAGCA	360
GTATTCTAGT GATAAGAATT CTTAACATAG CCAAGCGCCC CACGTTTGTT CCCCACGTTT	420
GTTCCCTTA TCTCGAG	437

(2) INFORMATION FOR SEQ ID NO:337:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 430 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GAATTCGGCC TTCATGGCCT ACCAAACCCA ATTTATTTAA AAANATACTT CTATATCATT	60
ATATGTATTA CCAATTGTTT TAGCCTTATA CAGGATGCGG TGTNCTGTGC TCCTTNGTGA	120
ATGTCNGTTG CTGGTAGCTG GTTATGCTCA TGATGATGAC TGGGTTGACC CCACAGACAT	180
GCTTAACTAT GATGCGGCTT CAGGAACAAT GAGAAATCT CAGGCAAAAT ATGGTATTTT	240
ACGGGAAAAG GATGTCAGTC CTGACTTGTC ATGTGCTGAT GAAATATCAG AATGTTATCA	300
CAAACTTGAT TCTTTAACTT ATAAGATTGA TGAGTGTGAA AAGAAAAAGA GGAAGACTA	360
TGAAAGTCAA AGCAATCCTG TTTTAGGAG ATACTTAAAT AAGATTTTAA TTGAAGCTGG	420
AAAGCTCGAG	430

(2) INFORMATION FOR SEQ ID NO:338:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 316 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GAATTCGGCC TTCATGGCCT AGAAATAGAT TTTTCCTCAG ACTCTCATCT CACATTCCCT	60
---	----

TTTAAGATTT CCTNGTCCTA TCCCCACCCC AGACGTTTCC ATTTTGCTTT TATTTTCTAT	120
AATAATTCCT GGGGGCCTCT ATTAAAGGCC TTTTCTTTG ACTACTTACA TCCATTATAC	180
CAGTATCTTT GTCAGTAAAA TTTTATATAT CTTTATTCT GTCATCAGGT TAAGAAACAA	240
TAATTGTATT TTAAAGGAA AATATTTTAC GATGCTACTA AGCAGTTACT TTGTCCACTT	300
ATGCAGGATA CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:339:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 306 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GAATTCGGCC TTCATGGCCT AGCTGGCTGG CACCTGGAGA ATCCCTGAGC TGGAAAAGCA	60
GCTTGGTCTG CAGAACTGAG TCACAAGACT GAGGCACTGG GGAGCCTCAG CCCCATCTGG	120
TTGTTGNTCC CTCTGTGACC TTGAGCTTGT CTTCCACTTG GTGCCGTAGG CCTTCATTTG	180
TCCATTGAAG TTAGCACCTG TCCCTCCCGT CCTCCAGAGA GGTCAGGAGG ATAAGCATT	240
GAAGACTCAC TGTGGTTTAT TGAGTGCTTA CTGTGCAGGT ACTGCTGTAG TTTTGTGCAA	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:340:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

CAAACCTTTG AGTNNNACAG TTAAGATATT ATGTGAAGCT CAGAATCATG TTTCAGACCA	60
TTGAAATTAC TGGTTAAAT ACAAATAGCT GAAGACATGA TGTAAGAT TAAGTACTTG	120
GTTTTGTAAC ATATTTACCA ATTAAAGTCA CAAAATATTT CTCATTATTT ATTCATGCAG	180
GTAAGTGA AAAAGATAGT GCAGAAATCA ACTTTAAATA AAAAATTATT CCTCCCCTTC	240
CTCCCACTCC CCTATACTCT ACAAATGTT TTCCCTGGGA CTAGGCCTTG AAAAGGCCAC	300
TACATATTAG TGTGACATGC ATTACTGTCT GCAATTAAAA AAGCTAACCT TGTGGTGATT	360
GTAATTACAT TATAAAAATG TCCACATGCA TAAATCTAAA AAAGGTTGAA AACCTACAGT	420
AAATCTACAA TATAGTGTTC ACATTTGACC ACTGGTTTGT GTTATGTAGA AGTCATAGAT	480
TTGGTAAAGC ATTGTAACAA TTTAGGAAGG CATCTAAATC TTTAAGTTCT GGACAAATTT	540
TATGTTTTAA TCTACAAAAT TGCATGAAGG CTAAGTCGAG	580

(2) INFORMATION FOR SEQ ID NO:341:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 433 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GAATTCAGAN TTNTGCTATG GTAGCACCAG ATGTCCAAAT TGAAGATGGG AAAGGAACCC	60
TCCTAATATC TTCCGAAGAG GGAGAGACGG AAGCTACTAA NTCACAAGAA GTTNTTCAGA	120
ATTTGGAATT AGAANTGGCA NCCGGCTTCA AGCAGATGAC TTCNTCCAGG ACTATACTTT	180
ATTGATCAAC ATCCTTCATA GTGAAGACCT AGGAAAGGAC GTTGAATTG AAGTTGTTGG	240
TGATGCCCGG GAAAAAGTGG GGCCCAAACA AGCTGAAGAT GCTGCCAAAA GCATAACCAA	300
TGGCAGTGAT GATGGAGCTC AGCCCTCCAC CTCCACAGCT CAAGAGCAAG ATGACGTTCT	360
CATAGTTGAT TCGGATGAAG AAGATTCTTC AAATAATGCC GACGTCAGTG AAGAAGAGGG	420
AAGCCAGCTC GAG	433

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GAATTCGGCC TTCATGGCCT AAAACTCTAA TAGTCTCTCT TCAGCGGAGC CACTGAAGGA	60
AGATAAGCCT GTCAGTGGTC CTAGGAACAA GACTGAAAT GGACTGACTC CAAAGAAAAA	120
AATTCAGGTG AATTCAAAAC CTTCATTCA GCCCAAGCCT TTATTGCTTC CAGCAGCACC	180
CAAGACTCAA ACAAACTCCA GTGTTCCAGC AAAAACCATC ATTATTGAGA CAGTACCAAC	240
GCTTATGCCA TTGGCAAAGC AGCAACCAAT TATCAGTTTA CAACCTGCAC CAAACTCGA	300
G	301

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GATTCAGATG GAGATGCCAA GCAGGCCCTT AGGTGAAGGA GTCTGGAGTC TGAAAGCATT	60
TGGGATGGGG ATATAGACTT GAGAGCCATC AGCTTATAAA TAGGACTTGG TCAAGAATGG	120
GTGGCCTCCA TCCTAGATGG ATATAAATA GAAATAAATA TCAATTTTTT TTCTTATAAC	180
ATTCCTAGGT TTTCATTTTT ATGACTTTAA GAAAAATATG AATGACAAAA ATAAACATA	240
AAATCAAATA TATCCGTATT GCCCTTTGGG GGACACCATC TCTTGCTCAC TTTACACAGT	300
AAGTGCCATT TCCTTCACCT CCATGGAAAA CATTTCGTAA ATTACTAAGT TGAATAACTT	360
AAAATATAGG ACGGGACATC TCGAG	385

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GCAGAAACCT TCAGGGAAAC CCCATGCTAG CGGCAACTGC ACCACACTTT GAGGAGAGCT	60
GGGGGCAGAG ATGTCGTCGA CTCAGGAAAA ATACAGGGAA TCAAAAAGCT CTAGACAGTG	120
ATGCTGAGAG TTCCAAAAGT CAAGCAGAAG AAAAAATCCT AGGTCAGACT TATGCAGTTC	180
CCTATGAAGA CGATCATTAT GCAAAAGACC CAGACATTGA AGCACCCAGC AACCAGAAGT	240
CAAGTGAAAC GAATGAAAAG CCAACGACAG CTCTTGCCAA CACCTGTGGA GAGCTCGAG	299

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GCATTTGGTT CTTTTATAT CTTCCTATTC TCTCACTATA TTCCTGTTTT TCTTTTAATG	60
CTTGACATC ATTAACTCG CTGTTATCCT TGTCTGTGAG TCATCTGGTC ATTTCTGTGT	120
GTTTTATTA ACTGATTATT CTCCTTGTCC TGGCCACATT TCTGTGCTTT TNGGCGTTTC	180
AGTAACTTCT GATTGGATGT TGGGTATTAT AAAGATTATA TTATTGAGTG TCTGGATTTG	240
GGGTGGTAGT TACTGTGGA TCAGTATGAT CCCTTTGAGG CCTATTTTGA AGCTTCAGCT	300
CGAG	304

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GAATTCGGCC TTCATGGCCT AGATTACAAC ACGTGTGCCA CCACACCTGG CTAATTTTTC	60
TATTTTGTAGT AGAGACGAGG TTTCAACATG TTGACCAGGT TGGTGGTCTT GAATTCCTGG	120
CCTCCAGCCT GGTGACAGAG CGAGACTCCA TTTCAAAAAA AAAAAACAAA CTTCATGCTG	180
AGAAGTCTGA AGAAAAAAA GATTTTAAAG AGGAAATGT GTAAGAAAAA TACTTCAGCT	240
TCTGTTACAA AATCAAAATA GAAAAAACA CAAATTTGGT GTTTCCTCGA G	291

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GTAACCTTAG CTGTACCTTG CAAACCAGAA CATATGGTCA CCCTACCCTC CGGTCACTTT	60
TTCTTCTTTG TTTCATTCT TTTAATTTT TTCCCTTTTA AACACACAGC ATTATCTTTC	120
CCTGAGCACC ATTGTCTTTG CAAATGCTCT TGCAATCGGG ATATTTTGA CCTGGCAACA	180
TGCATATTCA GTCTGAACAG TCTCTGTGAA CCTACCCCAA AACCTGGTTT TAGCTTCCAG	240

GCAGAAGACT CTGTTCCCTG GCTTGCAACC CCCAAACTCG AG

282

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GAATTCGGCC TTCATGGCCT ATATCAATGC AATTTTAAAT TTTTGTTAAT ATCAACAGCA	60
AAAGCCTAGT GCATTGGGAG ATGTGCAACC TCCCTGAAAA TCTTTTCTGT TTCTGGAGTA	120
CTTCAGGGGT GGCCTCTGGC CCCAGAGCCT TTGCCACAGT GCTCCCACCA GCCCCACCT	180
CATCCGCTCG TTTGCAGAGC CTCATCTACA GGTCCCACG CTGCCTTCTT TACTCACTCT	240
GCGCTTGGCC GTTTTGTTAT TTGGCTTAGT CTACATTGGG CGGAAGTCTG TGTGCACAGA	300
GTGGGTGTTT CTTCGAGCCC CTTCCTCTCA GAGGGCCACA CG	342

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GAATTCGGCC TCATGGCCTA CAAAGAGCTG GGATTACTGG TGTGAGCCAC CGTGCCCGGG	60
CTGGACATCT GGTTTAACT AGATGGAAGG GAAGAACATT ATGAATCTTT AAAATACGGC	120
TGTTGCCATT TTTCTCTCTT CTTAATATGC AGCATAGGTG ACAAGCTTTT CTGTCATCAT	180
CATGGAGCAT TCTGAATCAT GACATTTTGT TTTGAGAGTT CATTCTTGAA TTTTCAGTTC	240
AAAATATTGT TTGAACTATT ATTCCACATT CAAAGATTAT ATAAGGTCCT GTGCTTTTGA	300
ATCTTTTTCA AAAAATTAT TTCTGCCTGC TTAACAAAAA TACTTTTATT TCCCCACAGA	360
GAGTTCAGGA CTTAGATTA GTTTGTGTTT AGCTCACTTA ACTGGATAGA CAATTTTGCG	420
TTTTGCAACA CCATAGCTCG AG	442

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GAATTCGGCC AAAGAGGCCT AAAAAATGA AATTCCTTAT CTTGCATTT TTCGGTGGTG	60
TTCACCTTTT ATCCCTGTGC TCTGGGAAAG CTATATGCAA GAATGGCATC TCTAAGAGGA	120
CTTTTGAAGA AATAAAGAA GAAATAGCCA GCTGTGGAGA TGTGCTAAA GCAATCATCA	180
ACCTAGCTGT TTATGGTAAA GCCCAGAACA GATCCTATGA GCGATTGGCA CTTCTGGTTG	240
ATACTGTTGG ACCCAGACTG AGTGGCTCCA AGAACCTAGA AAAAGCCATC CAAATTATGT	300

ACCAAAACCT CGAG

314

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

GAATTCGGCC AAAGAGGCCT AGCTACCAGA GTGTGAGAGA CCATTGTCTC GTTGGCTGGC      60
GCTCACGGAC ATGCAGTCAC GGTAGCGGGA GCAATCACAA AACTGTAATT TACTTACCAA      120
ATCTCTTCTT TTCCGTAGCC TCGCCTGCCT GACTTAGAGA AAGAAAAGCA ATAATTTTAC      180
AGGCATTTTG AGGTGTCTCT TTGGGTTCTT TCTGTTTGAA AGGATATTTG TCGAAAAAAA      240
GAGCAAAACC GTTTTAAATA AACTCCCCCT GGAAAAAAC CCAAAACACT TGCATCTCGA      300
G                                          301

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(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

```

GAATTCGGCC AAAGAGGCCT AGCAAATACA CATTAATAAG AATGCCTAGA AGAGGACTGA      60
TTCTTCACAC CCGGACCCAC TGGTTGCTGT TGGGCCTTGC TTTGCTCTGC AGTTTGGTAT      120
TATTTATGTA CCTCCTGGAA TGTGCCCCC AGACTGATGG AAATGCATCT CTCCTGGTG      180
TTGTTGGGGA AAATTATGGT AAAGAGTATT ATCAAGCCCT CCTACAGGAA CAAGAAGAAC      240
ATTATCAGAC CAGGGCAACC AGTCTGAAAC GCCAAATTGC CCAACTAAAA CAAGAATTAC      300
AAGAAATGAG TGAGAAGATG CGGTCACTGC AAGAAAGAAG GAATGTAGGG GCTAATGGCA      360
TAGGCTATCA GAGCAACAAA GAGCAAGCAC CTAGTGATCT TTAGAGTTT CTCATTCCC      420
AAATTGACAA AGCTGAGCTC GAG                                          443

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(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

```

GAATTCGGCC AAAGAGGCCT ATAGGCNTCT TTGGCCGGCC AAAGAGGCCT AAAAAATCT      60
CAGCTATGGT TCATTATTAC TAGCTCAGCT TTTAATTCTT TAAATTGGTT GAATTATTCT      120
CTATGTCAGT TATTTTTATT GACCAGTTT GGAATATTTT TGTTCAATTA TCAGGGAGTA      180
TGCGGTAAAT GAAGTTGTGG CAGGGATAAA AGAATACTTC AACGTAATGT TGGGTACCCA      240
GCTACTCTAT AAATTTGAGA GACCACAGTA TGCTGAAATT CTTGCAGATC ATCCCGATGC      300

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ACCCATGTCC CAGGTGTATG GAGCGCCAAC TCGAG

335

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

GAATTCGGCC AAAGAGGCCT ACAGAGATTA TATTGGGGTT NCCATTTTGT GAAGCCANAG	60
ACATNTGGTC ATTGGGATGT GNGATTGCAG AATTATTTCT TGGANGCCCG NTNTACCCAG	120
GAGCCTNGGA GTATGCTCAG ATTCGANACA TTTCTCAGAN TCAAGNTTNN CCAGGAGNAC	180
AGTTGTTANA TNTGGGTACT AAATCCACAA GATTTTTTTG ACANAGAAAC AGATATGTCT	240
CNTTCTGGTT GGAGATTAAA GACACCGGAA GAGCATGNGG CAGAGACTGG AATGNAGTNT	300
TAAGAAGCCG GACTCGAG	318

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GAATTCGGCC AAAGAGGCCT AGTGGGAATT TTAAATACAA GATCCTGTTG AAAATATTGA	60
TATTCAAAGA AACAAACAGC TTTGGATCCA TAGCCACAAT TTAGGTTTTT CTAGATTAAA	120
ATCAGAAGTG ATTTTATTGT TGAAGATAC ATTAATTCTT TGAAGTCAGA ATAAGAGGCT	180
TGACAATTTA ATTTCTAATT AAGTGACTGA ATAGACAAAG GATCAAATAC AAACAGTAGT	240
GCAGGAAGAA AATAAATTGG AAGAAATAAT TGTTCACCA GTAGTAATAA TTAAGACCAC	300
CATTTTAAAA TTTTCTATAC ACAAAGAATG AGAAAATATT GTTATTATTA TTATACTTCT	360
TTCTTCTTCA GTATTAGTGG ACCCACATTA TCTCCTGTCA ATTCATTGTG TTTATNATGT	420
GAACCATCTC TCGAG	435

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GAATTCGGCC AAAGAGGCCT ACAGGCTCAC ATTGACTACA CACGTTTATA CCAGGCGCCA	60
TGTTCTTTGC CGAAACTCCC GCTCAGAGCC TGGATGATCT GCCCCTCACC TCTGCCCTCG	120
TTCCCATCCA CTCTCCCCTC CTGCTCTGT TCCTCGAG	158

(2) INFORMATION FOR SEQ ID NO:357:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

```
GAATTCGGCC TTCAAGGCCT ACTCTTCTTG GCATATTATT TTCCTGAATT GCTGCCTCTG      60
TTGTTCAAAC CATCCCGGAT TAATGACAAA AACTATCTT ATTCAAACCA AGAATTATCT      120
ACAACCTCC TTCTCAACTA GTTNNNGCAA GATCATTTCA GTTTTCTTT TTGTGCTACA      180
TCCTGGATTA ATTCTTCAGT TTNGTCTTCT CTGGAATCAC TACCTAAGGC TTATTCCATG      240
TTTCAAGTTT TTTGTTTTTT GTTTTTTTT ACTTTGATGA GTATGTTTAC CAACGCTCTC      300
GAG                                                                                   303
```

(2) INFORMATION FOR SEQ ID NO:358:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 493 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

```
GAATTCGGCC TTCATGGCCT ACAAAGTGTT GGAATTACAG GCGTGAACCTA CCGTGCCCAG      60
CCTTTTTTTT CATAGCAGTT TTATTAAGTT GTATTTGCCA TACCACCCAA TGTATCCATT      120
TAAGCACCTG ATTCAGTGGT TTTTCATGTA CTCATGGAGT TATGCAGCCA CAATCTTAGC      180
GCATTTTCAT TACCCAGAA AGAAACTGTA CCCATTATGC ACCCGGTTCC CNTCNTCCGG      240
TCNTGGCAAC CACGAGTGTA CTGTCTGTCT TCATGGATTT GCCTATTCTC GACGTTTCAT      300
TGGGATGAAA TCACACAGTG TATGGCTTCC AACTTTACT GTGCTGTTGT CAAGGTTTAT      360
CTATGTGTG GGTGCAGCCA CCCCTTGGTA TCCACAGGGA TTGGACCCAG GAGCCTGCAC      420
CGATCCCTG CAGGGATGCC TGTGTCCAC AGTGCCCCCT GCAAACTCA CTGATATGAA      480
GAGTCGGCTC GAG                                                                                   493
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(2) INFORMATION FOR SEQ ID NO:359:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

```
GAATTCGGCC TTCATGGCCT AGTTAACATG ACACAAAATC TTTACCTGCA GTTCTAATAT      60
TTTGCAAGGC TGAAGTCCAT ATTTACAAC GTCTTAGATC ATCTCAATCT GATTATTTAA      120
CTATTCTCTC TAACTGCTAG TCCAGCCCCCT AAAACTGCAT TTCTCTGCTC CTCCAAAGCT      180
TAGTGGCTTA TTGAAGTCCA TATTTGCATT GTGACAGAGC CAACTCCCA GAATGGATTG      240
CCACTCAGTG TAATGCAATA GGAGCACTTT AATTTATCT CCATTTTCTG GACCCAGTGC      300
ATCATTCTAG CCTTTTTTTC TTGGAATGAA GTCTGGCTGA GAATGATGAT CCATTAGTAA      360
GAATTACTTA ATAAATCAAC TCTTGGTTAT GAGTGGCAGA AACTAAAGC CAGGCTCGAG      420
```

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

```

GAATTCGGCC TTCATGGCCT AATGTCACCA CTGTGGAAAA CCATATAGGT CGAAGGCTGG      60
ACTTGCATAT CACCTGAGGT CAGAGCATGG GCCTATATCC TTCTTTCCAG AGTCAGGACA      120
GCCAGAGTGC TTAAGGAGA TGAACCTAGA GTCAAAGAGT GGGGGCCGAG TTCAGAGACG      180
TTCTGCCAAG ATAGCTGTAT ACCACCTACA GGAGCTGGCC TCTGCTGAAC TGGCCAAGGA      240
ATGGCCCAAG AGGAAGGTGC TTCAGGACCT GGTACCTGAT GATCGAAAGT TAAAATATAC      300
TCGTCCAGGG CTCCCTACCT TCAGCCAGGA AGTACTACAT AAATGGAAGA CTCGAG      356

```

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

```

GAATTCGGCC TTCATGGCCT ACATGATGAA ATGTTGGCTA AAAGAGTCAC CCTAATATTA      60
ATAAAATGTT TTATTCTTCA TGTGACTAAA TCAGTGTGCA TGCAAGAAAA AGAAAGAAAA      120
AATGCTTAGA TTCCTTTTTT AAATTATCTC CAGAATTCTT AATTTTTATA AATTAAGGAC      180
CAACAAATCC CATTTTGTTT TCACGTTTGA CATTTGTTC TTTGACTTAA ATAACCTCTC      240
CACTCTTTAT TTTCTATTT GTGGTGATT GAATAATTTT TCAGAAAAATA TGTACTTTCT      300
GATAAATTGT AGTGTGTGAG TAATGAAAAC TGCTCTATGG TGCTCCCCTC GAG      353

```

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

```

GAATTCGGCC TTCATGGCCT ACGAACTACT CTAAGTAATG GGCCAAGTCA TGAGCTGCAC      60
AAAGGCCCCC AAGACCCAGA CGGGTTTAAT GTTAAGCAAA ATGCCGCCTG GTCTCAGGTA      120
GACACTCAGC CACCGCTAGC CCCAGTCAAC TGTCCTATGG GAAGGCAGAA GGCCCGGTGT      180
TGCCAGGTCT TAAGTTTCA GGAGGAAATC CTTAAACGAT GGTGTTTCAC TATAATGGAT      240
TCATTTTTAT GTTTTATAAA TCTCTATGTT CATGTAAGT TATTAGTACT TTTATGTGAT      300
AAAATCTTTT TTTTAAACAT TGGTAATCA AAAACACAAC ACCCACATAC ACTGAGGACC      360
AAACAAAACC CGTCTGCAAG CAGGCTCTCT CCGAG      395

```

(2) INFORMATION FOR SEQ ID NO:363:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

GAATTCGGCC AAAGAGGCTT ACAAAGGACA GCCCTGTCTG CACACTGAGT TACTGTGGAT	60
TTTAAAGAAA CTTTCGCTAAA GAATTTAGGC ATTCTGATT CAGTTAAAGG ATTGCCAATT	120
CATCAGTCCC TGAAACTAGA GCAATCTCAA CAGGACAAGA AAAGAAAATG GGCTTTTAA	180
GTCCAATATA TGTCTTTTC TTCTGTTTG GAGTTAGAGT ATACTGCCAA TATGAAGCTT	240
ACCGATGGGA TGACGATTAT GACCAAGAGC AAAATGTCTGA G	281

(2) INFORMATION FOR SEQ ID NO:364:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GAATTCGGCC TTCATGGCCT AGTGCCACTG CACTCCAGCC TGGTGACAGA GTGAGNCTCC	60
GTCTCAAAAA AAAAAAAAAA AACTCAGCTT CTTTCAGAGAG ATAAAATTGG GGGAGGAGCC	120
CAGGGCCACA TACCAAGCTT TGGGACATGG TGCCTCATGC TCTCTGGGAT TGCAGACCAT	180
CCAGGTCTGT CTTGCCCCCT GTTACTGCAC ATATATCCAC TCACATGTCT TCCCTCAGGC	240
TATCGGGCAG GGGGACTTCA CCAGGGGGTT TATGGATAGG CTCAAGAGG GTCTGTGAGC	300
CCCCAGAAAT TGTGTGTGAG ACTGAGTATG TGTTCTTTT TCCAGGAAAT TCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:365:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GAATTCGGCC TTCATGGCCT ATTACAATAT GCTTAAAGCT CAAAATGATC GAGAAACACA	60
AAGTTTGGAT GTCATATTTA CTGAAAGACA AGCGAAAGAA AAACAAATCA GAAGTGTCGA	120
AGAAGAAATT GAACAGGAAA AACAAGCAAC AGATGACATT ATCAAAAATA TGTCTTTTGA	180
AAACCAAGTC AAGTACCTAG AGATGAAAAC CACAAATGAG AAAGTGTAC AGGAATTAGA	240
TACACTTCAA CAACAATTGG ATTCACAGAA CATGAAAAAA GAGAGCCTGG AAGCAGAAAT	300
AGCTCACTCC CAGGTGAAAC TCGAG	325

(2) INFORMATION FOR SEQ ID NO:366:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 549 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

```
GAATTCGGCC TTCATGGCCT AGTGAATTGA GTTTGTGAAA CCTCCTTAGC ATATCACACA    60
ACACTAATTT TCCACTCTCA ATATGTGGCT GTAGAGTGTT TAATGTTTAC TTTCATATCG    120
CTTTTCCATA GTAGTGCAAG ACCTCAGTTT AGCTTGTTTA CATTATTTGC AGATTACTT    180
ACAGTGTAAT ATTTATTTCT GTTTAAATA GTGTTTGCAA TAGGAGAAAA TCATATGATC    240
TTAAGCATAT ACACCAAAGG TAAGAAAGGA AGCCACTATT GTATCTTTT GATGAATTCC    300
AGATGAGCTG GGATCAAATT GAACTGCTTA GGCAGAAATT TAAGAGACAA GTAGAAGTGG    360
TGCAGAAAGA CATTGTGACT GCAATGTCCT ATTTACAGCT ACTGCCCGA GGAGAACT    420
CCCAACATGA CAAAGAGTTC ATCAGCTTGA ATGTTAACTT TTGAAAACAA TTAATGAGC    480
CACTGCACCC GGCCAATCTA GTGAATTGAG TTTGTAAAC CTCCTTAGCA TATCACACAA    540
CTACTCGAG                                     549
```

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 481 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

```
GAATTCGGCC TTCATGGCCT AGGAGGCGGA GGTGTCAGTG AGCCGAGATC ACGCCATTGC    60
ACTCCAGCCT GGGCGACAAC AGCAAGACTC CATCTCAAAA AAAAAAAGTG AGATCCTGCC    120
GATGGGCCCCT TCCTGTCCAC CTGTCAGGAA AACCTGCAA AGGTTCTTGT CGCACCATTA    180
GAGCCAGTTT TTCCCAAATG ACACCCATAC CTGATTTTCC TTGTTCTTCT AAGACAGTTT    240
TAATTAGGAT AATCTCATAA GTGCTACATT TTCAGTGAAT TTTTCAATAT AGTGGCCCAT    300
GTTCTTTCTT TTTTTTTAAA GTCTTTTTC TCTGGTAGCA CATGTGATTT AATGCTTGCT    360
TTCTGAATT GTAGAAATAA AAGGAAATCA CAAGTATTTT CCAACAAAGT GGAAGTGGG    420
CCGAAGGGTG CAGAAAAAAA CTATAGAAAT TAGTTAAAAA TTAGGAAGGG GCAGTCTCGA    480
G                                     481
```

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 285 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

```
GAATTCGGCC TTCATGGCCT ACCAACTCAG AAGGGAATGG AATGTGGAAA AAAAGAAAGA    60
AAACCTGAGT AACTTTTCCT AAAAAAGTCT AGCTGTTCTC AGTTGTGGC ACCAAATGGG    120
GAGCAGGGAA GTTCCAGTC GCAACTGACT AATTAGCCCA ACCCTNATTT ATTGATAATA    180
ATAATGATAA ATAATAATGC TAGCTAACAC TTAGTGAGCA AATACTAGGT ATTATGTGAA    240
ATCATTCTCT TGTATTAAT CACTTAATCT ACACAGCAAC TCGAG                                     285
```

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```

GAATTGGCCT TCATGGCCTA NGTGTGGATA GTGGAGGCAT TGGTAGCCAG AACATGTCAC      60
TTTATGACAG CATATGGACA GCAATATGGA AGCCCAGCAT GGTGGGTAAA AAATGGGGCA      120
GCCTAAGGTC AATGACTTTT GGCTGAGTCT GTGAAGATCT CAAAGCTTGG TGGTTTTTAG      180
CATAGCCTTT ATACCATACT TAACTCCGGG TAAGGACCAG GACCACTGTA GCGACCAATT      240
GATGACAGA GTAAAGTATG TGGGTTTTTT TTTTCCCCCA ACTGGGCTGA TTCTCTTAGA      300
ATAAAAATTG TATACCATTA TATTATGTTA ACTTGATCAC AAAGAACAAA ATGTTATTTA      360
TTAATAATAT AGCATTGTCA TCTGTTTGAT GAATTTTCTT GATTTAATGC TTGTTTAGAT      420
TCAGTAAGCC ATTCTCAGGA ACTATAATAA ATGCTTCTTC CAACTTCTCG AG              472

```

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```

GAATTCGGCC TTCATGGCCT ACGAGTGCTT GCTGGAATCG TTTACCCTNG TTAATTTTTA      60
TCATNTCCTC TTTATGAGCA TGATATGGCT TCAGCTGTTC CACTTTGATC CAGGCATGAT      120
CTTCTGTTCC AAAAAATTTC ACAAAGAAGC ATTTCTTTCC GCGAGGTTTC TTCAAGTCCT      180
TTGGTGGATT AACAATCTTT CCTGGCCAAG GAGGATATCG GCCGAGTTTC CCCACACCA      240
AGTCGCCGAG CCGCAGACTC ACAGCCGCCA TCTTACCACC CAACCACCGC CGACGCACGG      300
GCCGCCG                                           307

```

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 414 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```

GAATTCGGCC TTCATGGCCT ACAACGATCT TGTCTTCTTC TATCAGGTTT GCGAAGGTGT      60
TGCGAAGGCC AGCCATGCCT CCCACACAGC TGCCAGGCT GGGCTTCCTG ACAAGCTTGT      120
GGCTCGTGGC AAGGAGGTCT CAGACTTGAT CCGCAGTGGA AAACCCATCA AGCCTGTCAA      180
GGATTTGCTA AAGAAGAACC AAATGGAAAA TTGCCAGACA TTAGTGGATA AGTTTATGAA      240
ACTGGATTG GAAGATCCTA ACCTGGACTT GAACGTTTTT ATGAGCCAGG AAGTGCTGCC      300
TGCTGCCACC AGCATCCTCT GAGAGTCCTT CCAGTGTCTT CCCCAGCCTC CTGAGACTCC      360
GGTGGGCTGC CATGCCCTCT TTGTTTCCTT ATCTCCCTCA GACGCAAACT CGAG              414

```

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```

GAATTCGGCC AAAGAGGCCT ACTGGATGGC ATCTACTTCG TATGACTATT GCAGAGTGCC      60
CATGGAAGAC GGGGATAAGC GCTGTAAGCT TCTGCTGGGG ATAGGAATTC TGGTGCTCCT      120
GANCATCGTG ATTCTGGGGG TGCCCTTGAT TATTTTCACC ATCAAGGCCA ACANCGAGGC      180
CTGCCGGGAC GGCCTTCGGG CANTGATGGA GTGTCGCAAT GTCACCCATT TCCTGCAACA      240
AGAGCTGACC GAGGCCCAGA AGGGTTTCA GGATGTGGAG GCCCAGGCCG CCACCTGCAA      300
CCACACTGTG ATGGCCCNAA TGGCTTCCCN GGATGCAGAG GAGGCCCAAG GACAAAAGNA      360
AGTGAGGNAG CTCGAG

```

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

```

GAATTCGGCC AAAGAGGTCC TGTAAGTATG ACTATTTAAT TTATTTCTTT TCACAATATA      60
AAAAGCACAT GCCATATTTT GAAAGACTAT TAAAGGTGGG GACAAGAGGT TATTTAAATC      120
TATGTTTGGA TGCAACTTTT ATGGCTTAAA CTACAAAGAA TTATCCTTTT TATATATTAA      180
ATGATTGTAT AGTTCTTTTA ATACTGTTTT TTGATACAAG TGTGAAATNC TTAAAGAAAA      240
TGGCAAACAT CACTAACAAAC CATTACAATT CTAATAGCTA ACTTTTCTGA GCCATTACTT      300
GGAACCATGC ACTGTTTAAA ATGCCTCACT TGGCCAATGC TCGAG

```

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

```

GAATTCGGCC AAAGAGGCCT AAAATGCGGA GTTATAATCC AGAAGGGGAG TCTTCAGGGA      60
GATACCGAGA AGTAAGGGAT GAAGATGACG ATTGGTCCTC TGATGAATTC TGAAGATAAT      120
CTCCTAAATC ACTGACGTTG AGATGTCATC ATCTTACATC AGACTTTCTA ACTAGTATCA      180
AGATCAGTGT CAGATATTGT TGAGGGAAGT AATTTTATAA AGTTACACAA AGGTAGTTAT      240
AAAAAAGCC CAGTTGTCTT TTCAGAAAGT GACTTTCATG TGCTTGAAAA GTTTAATATT      300
TGAATATTGT GTTTAACCAC ATGGTATTAA AATTTTGCAA TATATTGTGT ATTGGTCTGA      360
TATTTTAGTA TATAGTAGAA CATACTTTT TTTTCTTTAA GCCAAATGAA AAGAGGTAAC      420
TTTGCTTTT TCCTTTTCT TACCTATCAA ATAGCATTTA TTACATGTCT TTCAGTGAAA      480
TACTTAGTTG TTCCAGGCAC GCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

```

GGAACGAATA GAAGTGTGTTG TATCTGTGGG TTNGACACAC TACTGAATCA CAAAGTCTTT      60
GGAATAATTC TCAAAGCCA TCACTTTTAG CCCACTTTCT CATTCAATTA TGCTCTATTC      120
TTTTTCTAGC ATGTCTAGCA GAATCTCTT GAATCTTGC AGTGAATTGG TGCTCCTTAA      180
ATACCTGCTA TTTTGAATA GTTTTGACTT AAATACATTT TCCTTTTCTC CCAGTTGCAA      240
AATGTCAGGG CTGACAACTG AAAGGGCTTC TGAAGATTGT CAGTGTTCTC ATATTCAGAT      300
AGGTAGCAAA GAATCTGACA CATTTGGTAT AATAAACCCA CTCGAG                      346

```

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

```

GAATTCGGCC TTCATGGCCT AGGATGAATG ACCTTAAAGA TCGAACATGA ATAAGAGACA      60
TCATTTACCC TCAAAGAAAC TAGAGTCTGA TTGGGCAGGG AGGAAAAGGT ATTAAAATTA      120
TGTCTTTCTG CATTGTGTGG ATTTGAAGTT TGTTTTTGT TGTTAAGAGT CTTATTATTA      180
GGATAATGAC ACTGTTTTTT CTTTATTAAG TTA CTGTGTG GGCAGTTAAG ATGATTCTGG      240
TGGCTCTTAA CATTTTTTTT TTCTCCAGTC GGGAACATGC CCTGTGTGCC GCCGTCATTT      300
CCACCTGCG GTTATTGAAG CATCTGCAGC TCCTTCCTCT GAGCCTGATC CTGATGCCCC      360
ACGGTCTCGA G                                     371

```

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

```

GAATTCGGCC AAAGAGGCCT AGGAACTGTT CTGTTGAAAA TACCCATCCA ACAGTTTCTT      60
ACTATGCTCA TCCCCAAGTG GCATCCTACA ATACCTACTA CCATAGCCCT CCTCACCTGC      120
CACCATATTC TGCTTATGAC TTTCAGCATT CCGGTGTCTT TCCATCCTCC CCTCCCTCTG      180
GACTTTCTGA TGAGCCCCAG TCTGCCTCTC CCTCACCCAG CTACATGTGG TCCTCAAGTG      240
CACCGCCCAA AACTCGAG                                258

```

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

```

GAATTCGGCC AAAGNGGCCT AATATAACTT AGCTGCTATT TACAACACTA GAAATTTAGT      60
ACTTTAAGTA ATTTACATC  TATGATAACA TTTGTTACTT TATTTTAAAT GATTTTTTTA      120
CAGTAGTTAT GACAGTAGGA TGGTTATGGA ATTGGAATTT AAACCTCCAA CTAATGAGCT      180
TAAGCTGCTT GGAATATTAA TTATGTAGTT TTTACATTCC ATTTTAAAC AAAAAGCTAG      240
NAAAGGTGCT GGCATTCTGA GGCCTGCAAT TAGGCCACAT AGCAGAAGCT TGCTCCTTCC      300
TTATCTGGGT GAAATATTTT ATTTTTCAC TTTGAGTCAT ATTCCCACCC CTGTATAAGC      360
TACATAGGAG CCGAATGAA  TTGGGTAGGA AAGGAAATTA TGCAACAAG  TCTCAGCTAG      420
TGCTGAATGA CTCGAG                                     436

```

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

```

GAATTCGGCC AAAGNNGCCT AGCACATGCG TCCCCGCAGT TGTCTCTTC TCCTTTCCAA      60
GTTCTGNCT  CTAAGGAGAT GGAAGTATTC TAAATTTTCC TACTTCTAAT TTTTACTATG      120
CAACCAGCAA AGCGGGGAAG GTTGCAAGGA AAATTGTCCG GTCTTTCACA ACTAAGNNGG      180
AAATTACTTC TCCTATGTTT TTATTCAAGA GTTGTCTTTA AAAGTGCCTG CCGGCTTTCC      240
CTTTTAACTT TTAGGATTAT AGTTAAGGTT ATGGAAAGTA GTCATTCATT AGTTCAGTAC      300
GTTTCATATA GTTCTCTAAC ATAGAAGAAA ACTCAGTCAC CAGACAGTGA AGTCATTTAG      360
CAGTGGTTAT TGGAAGATAA TCCACAGTGA TGGTAATGGA ATACTGGAAA CNCATCCTAA      420
ATAATCTGTA ATTATTATTA TTATTATTTT GGGACAGNGC GAGGCTCCGT CTCCAAAAAT      480
AAATAAATAA AATAAATAAA TAAATAAATA AATAAAGGAT GGTGCACGTC TCGAG        535

```

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

```

GAATTCTAGN CTGCCTCGN GTCGCACCCA TGTTCAATCG TTCCTTCCTT CCTTCCTACA      60
TTCTTTTTTT TTNCCTTCTT CTCAGGGTC TCACTCTGTC ACCCTGGCTC GAG          113

```

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 660 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

```

GAATTCGGCC AAAGAGGCCT ACACACATCG TTCATGTACA TGATCGCCGG ACTCTGCATG      60
CTGAAGCTCT ACCACAAGCG GCACCCGGAC ATCNACGCCA GCGCCTACAG TGCCTACGCC      120
TGCCTGGCCA TTGTCATCTT CTTCTCTGTG CTGGGCGTGG TCTTTGGCAA AGGGAACACG      180
GCGTTCTGGA TCGTCTTCTC CATCATTAC ATCATGCCA CCCTGCTCCT CAGCACGCAG      240
CTCTATTACA TGGGCCGGTG GAAACTGGAC TCGGGGATCT TCCGCCGCAT CCTCCACGTG      300
CTCTACACAG ACTGCATCCG GCAGTGCAGC GGGCCGCTCT ACGTGGGACC CATGCTGCTG      360
CTGGTCATGG GCAACGTCA* CAACTGGTCG CTGGCTGCCT ATGGGCTTAT CATGCGCCCC      420
AATGATTTCG CTTCTACTT GTTGGCCATT GGCATCTGCA ACCTGCTCCT TTACTTCGCC      480
TTCTACATCA TCATGAAGCT CCGGAGTGGG GAGAGGATCA AGCTCATCCC CCTGCTCTGC      540
ATCGTTTGCA CCTCCGTGGT CTGGGGCTTC GCGCTCTTCT TCTTCTTCCA GGGACTCAGC      600
ACCTGGCAGA AAACCCCTGC AGAGTCGAGG GAGACAACC GGGACTGCAT ACCCCTCGAG      660

```

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

```

GAATTCGGCC AAAGAGGCCT AGTGTGGGA GCTGTGGGCT GTGCCCTTCC AGTCCCCCAG      60
AGCAGTGTG TTGCCAAGA ATCTCCTAGC GAGAGACCAG GGGCTACTGC CAGGTGACAG      120
AAAAGGGAAC ATCAGTTCCG CTATACCCAC AGCTCACCTG GCGGCCTGGG GCCTGCACAG      180
GGCCTGGTTG AGGCAGTGA CCCCATTTTTT GGGCCGTCTG TGGAGTTGAT GTTCTGCCA      240
GCTGGTCCCT CTCTGTCTTC CCTGGAACTT CACCTGCAGT TTGATGCCTG AGTTAAAATT      300
GTTCTTCTAA ATAATCACT GTAGACTTTC TGTTTTTTAGC TATGTGAAAA CTTCTGAGAA      360
ACTGGAGAG TCTCGAG                                     377

```

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

GAATTCGGCC TTCATGGCCT ACTGGGCGGT CTTTGCAGCA ATAACAATAT CTGCTCCATC      60
CTTTGCTGCT TTCAATGCAA TAGCTTTGCC AATGCCACGG CTGACACCTG TGATAAAAAAC      120
TGTACATCCT GCCAGCCTCC CGGTGTGGG TAACATGACT TTCGTAGATC AGAGGAGGCG      180
GCGGGCGAAG CGCACGTCGA GCGGGGAGC GGCGCTGCCT GTGGAGATCC GCGGAGGCCG      240
ACAGGATTCT TTGGCTGCCG TCCCCGCTGC TGTGCATTGG GTTAAAAACG ACAACCAACT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```

GAATTCGGCC AAAGAGGCCT ACTTATTTTA CACAGCTTGA TTAAGGTCTA TGTCGGTATA      60
ATTTTTTTTA TGAGTCTNAC ACGTGGGATT GTTTGAGCTT CTTGAATTTG TATGTTTATA      120
CAAAATTTAGG AATTTTTTTC ATCCATTATT TATTTGAATA TATTCTCTGT CTTCAGTGTC      180
CTTTGAGGAC TCCAATTACG CATATACCTA ATTGCCTGGA GTTGTCCCAT AGCTTACTGA      240
TGCTTTGTTC ATTTTTTTCT TTCTTTTCTT CTCACCATGC TTTAGTTAGG ATAGTTTTTA      300
TTACTGTTTT TTTAAGTTTG CTAATCTTTT CTTCNAGCAT GCCAGCTCGA G              351

```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

```

GAATTCGGCC AAAGAGGCCT AGCGTCTTGG ACATGCCAGG AATAAAAAGG ATACTCACTG      60
TTACCATTCT GGCTCTCTGT CTTCCAAGCC CTGGGAATGC ACAGGCACAG TGCACGAATG      120
GCTTTGACCT GGATCGCCAG TCAGGACAGT GTTTAGATAT TGATGAATGC CGAACCATCC      180
CCGAGGCCTG CCGAGGAGAC ATGATGTGTG TTAACCAAAA TGGCGGGTAT TTATGCATTG      240
CCCGGACAAA CCTGTGTAT CGAGGGCCCT ACTCGAACCC CTACTCGACC CCCTACTCAG      300
GTCCGTACCC AGCAGCTGCC CCACCACTCT CAGCTCCAAA CTATCCCACA TATCTCGAG      359

```

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

```

GAATTCGGCC AAAGAGGCCT ACTACATGTA AAACACTTTT ATTCATTAAA AAGAAAACCTG      60
ACTGGCTTGG ACCTACAAAT TAGTTTCATT ATTTGTTAAT GTTTGAAAGC CATTAAAAGA      120
TGAATATTAA GGTTTCTTTA TACTCAATAC TTGTAGTTTT GTTTGGGGGA ATGAGAGGAT      180
GCCCTTG GTA CTTTGTGAG GCCTCTCCAC TGAGGGTCAA TCATGACTTC TGTTTTAAAC      240
CAGCCCATCC CATCTTCTCC AGCTGCTCTC CTTATGTCTT GCTTCTCTCC CCTCCAACTT      300
TCTCAGCACC AGGACTCGAG

```

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

```

GAATTCGGCC TTCATGGCCT AGTGGGAGCT ATTTTCTTTT TTGTGCATAT AGATATTTCT      60
TAAATGAAGC TGCTTTCTTG TCTTTTATTT CTAAAAGCCC CCTTATACCC CACTTTGTGC      120
AGCAAAGATC CCCGTGCAGG TCACAGCCTG ATTTGTGGCC AGGCTGGACA AATTCCTGAG      180
GCACAACCTG GCTTCAGTTC AGATTCAAG CTGTGTTGGT GTTGGGACCA GCAGAAGGCA      240
AACGTCCAGC CAACACACAG GACTGCAAGA GGTCTCGAG                               279

```

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```

GGTAGAAGCA GGAGGTTTTC AACCTAGTCA CAGAGCAGCA CCTACCCCTT CCTCCTTTCC      60
ACACCTGCAA ACTCTTTTAC TTGGGCTGAA TATTTAGTGT AATTACATCT CAGCTTTGAG      120
GGCTCCTGTG GCAAATCCC GGATTAAAAG GTTCCCTGGT TGTNAAAATA CATGAGATAA      180
ATCATGAAGG CCACTATCAT CTCCTTCTG CTTGCACAAG TTTCCTGGGC TGGACCGTTT      240
CAACAGAGGC TCGAG                               255

```

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

```

GAATTCGGCC TTCATGGCCT AGGCCACAT AGAAGAAATG AATGAAAAGA CTTTAGAAAA      60
GCTTGATGTG AAGCAAACAG AACTAGAATC ATTATCTTCT GAACTGTCAG AAGTATTAAA      120
AGCCCGTCAC AACTAGAAG AGGAACTTTC TGTTCTGAAA GATCAAAACAG ATAAAATGAA      180
GCAGGAATTA GAGGCCAAGA TGGATGAACA GAAAAATCAT CACCAGCAGC AAGTTGACAG      240
TATCATTAAG GAACACGAGG TATCTATCAA GAGGAACTCG AG                               282

```

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATTCGGCC	TTCATGGCCT	AGATAGAGCT	CAAAAACATG	GCATGGATGA	ATTTATCTCT	60
TCCAACCCCT	GTAACCTTGA	CCACGCTTCC	CTCTTTGAGA	TGGTACAACG	CCTTACTTTG	120
GATCACAGAC	TTAATGATTG	CTATTCTTGC	CTGGGCTGGT	TCAGTCCTGG	CCAGGTGTTT	180
GTAAGTAGAC	AGTATTGCGC	CCGAAATGGA	GTCCGGGGGT	GTCACCGACA	TCTCTGTCTAC	240
CTCAGAGACT	TGCTTGAACG	GGCAGAAAAT	GGCGCCATGA	TCGACCCAC	CCTTCTTCAC	300
TACAGCTTTG	CCTTCTGTGC	ATCCCATGTC	CATGGGAACA	GTCAACAAAT	GCATGTGTAC	360
CTTAGTGGGC	TGCCACCAAA	TACAGACCAC	GGTTCTTCCC	TATAGTGAGT	CGTATTAATT	420
TCAGAGGAGT	ATTAGAAGA	GAAGCTGAAG	CTGTCGAG			458

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 366 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAATGGGACT	CCAAGCCTGC	CTCCTAGGGC	TCTTTGCCCT	CATCCTCTCT	GGCAAATGCA	60
GTTACAGCCC	GGAGCCAGAG	GAGCGGAGGA	CGCTGCCCCC	AGGCTGGGTG	TCCCTGGGCC	120
GTGCGGACCC	TGAGGAAGAG	CTGAGTCTCA	CCTTTGCCCT	GAGACAGCAG	AATGTGGAAA	180
GACTCTCGGA	GCTGGTGCAG	GCTGTGTCGG	ATCCCAGCTC	TCCTCAATAC	GGAAAATACC	240
TGACCCTAGA	GAATGTGGCT	GATCTGGTGA	GGCCATCCCC	ACTGACCCTC	CACCTCGAGG	300
TTCTCCCTAT	AGTGAGTCGT	ATTAATTTTC	AGAGGAGTAT	TTAGAAGAGA	AGCTGAAGCT	360
GTGCGAG						366

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GGCGGGTGGG	GGTTAATTAT	CTGAAACCTA	CTAAAACGGA	CTACAGTTAT	CTCTAGGCCAA	60
TGCTGTTGGA	GTGTTTCCTG	CAAATGCATT	TCACTCATTT	TTTGTGATT	ATTTTATAAG	120
TATACTGGGG	CAAAAATTTT	ACATTCTAAA	TTGTTCTTAT	TTATTATTTT	TATTATAGAT	180
ATATGAGGAT	ATTACTTACT	CTATTACACA	TATAATTTAT	CTTTTAAATT	TTCAAGTGAG	240
TTCTACAATT	AACTTTATCA	TCTAAATTCT	CATTACAGAT	AGCATTTTAA	TGTCCAGAAA	300
GAAAAAAGG	TTTTTTATTG	TTATATGTGA	AACCATAAAA	ATATTACCAG	CTTGTGGCCG	360
GGCGTGGTGG	CTCAGCCTTA	TAATCCCAGC	ACTTTGGGAG	GCCGAATCAC	CTGAGGTCAG	420
GAGTTCAAGA	CCAGCCTGGC	CAACATGCGG	AAACCCCGTC	TCTACAAAAA	TGGAAAAATT	480
AGCCCGGCAT	GATGGCAGGT	GCCTGTAATC	CCAGCTACTC	GAG		523

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 548 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GAATTCGGCC TTCATGGCCT ACCCAGATGA AACTTTTGGG GGGAGAGTGC CCAGACCAGC	60
CTTTGTCCAC TATGACAAGG AGGAGGCATC TGATGTGGAG ATCTCCTTGG AAAGTGACTC	120
TGATGACAGC GTGGTGATCG TGCCCGAGGG GCTTCCCCC CTGCCACCCC CACCACCTC	180
AGGTGCCACA CCACCCCTA TAGCCCCAC TGGGCCACCA ACAGCCTCCC CTCCTGTGCC	240
AGCGAAGGAG GAGCCTGAAG AACTTCCTGC AGCCCCAGGG CCTCTCCCGC CACCCCCACC	300
TCCGCCGCCG CCTGTTCTG GTCCTGTGAC GCTCCCTCCA CCCCAGTTGG TCCCTGAAGG	360
GACTCCTGGT GGGGGAGGAC CCCCAGCCCT GGAAGAGGAT TTGACACTTA TTAATATCAA	420
CAGCAGTGAT GAAGAGGAGG AGGAAGAGGA AGAAGAGGAA GAAGAAGAAG AGGAAGAAGA	480
GGAAGAGGAG GAAGACTTTG AGGAAGAGGA AGAGGATGAA GAGGAATATT TTGAAGGGGT	540
TACTCGAG	548

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 577 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GAATTCGGCC TTCATGGCCT ACTTACTAGG AATTAAAAGA CGGATTTCCA AGGAGATTCA	60
GAGGCAGCAA GCACTACAGA AGTCAGAACT CCAGCACCAT CTGCTCCGTT TCTTGAAGTT	120
TGCTGAACGA GGAATCACAG CTGCAACGTG GGGTGATTGT ATTGATCAAA ACCCACTGGG	180
AAGSACAAAG AGTTTGCCGC CTTTCGGGGA TCCAAGGGAC TGTGGCGACC GTGCCTCTGT	240
GCCAGCGTCC CAGGAAGGAA GCCAACCCTG AGCGAGCCTG TCCTCTGTGG CAGGTCCACA	300
CGGTGTGGGT GGGCAGGGCT TGGACCCCG TCTCCATGGC AGGTCCATAC AGCATGGGTG	360
GCAGGGTTTG GACCCGCCCA GCAGCACCAC GGACCCAGC CACTCTCGGG GGCAGACGTC	420
AGAATCCGTT CCGAGCAGC TCCCGTGCCC TGGGGGCAGT CACAGAGCCC CCCAACACCC	480
CCGTGCTCTG CACCAGCCTC TCCCTCCACA CCCGAAGCAG GCGTCCATCT GTGTCCTCCT	540
GGCAGCCCTT CAAACACACA CCACCCATA TCTCGAG	577

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GAATTCGGCC TTCATGGCCT ACATCTTCAT TGCTGAGGTT GCAGCTGCTG TGGTCGCCTT	60
GGTGACACCA ACAATGGCTG AGCACTTCCT GACGTTGCTG GTAGTGCTCG CCATCAAGAA	120
AGATTATGGT TCCCAGGAAG ACTTCACTCA AGTGTTGGAAC ACCACCATGA AAGGGCTCAA	180
GTGCTGTGGC TTCACCAACT ATACGGATTG TGAGGACTCA CCCTACTTCA AAGAGAACAG	240
TGCCTTTCCC CCATTCTGTT GCAATGACAA CGTCACCAAC ACAGCCAATG AAACCTGCAC	300

CAAGCAAAAG GCTCACGACC AAAAAGTAGA GGGTTGCTTC AATCAGCTTT TGTATGACAT 360
CCGAACTAAT GCAGTCACCG TGGGTGGTGT GGCAGCTGGA ATTGGGGGCC TCGAG 415

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCGGCC TTCATGGCCT ACTAAAAGAT ACTTCAAAGT GACAAAAACG TGTCCTTCC 60
CCACTTAGAG ACAATGATTA ACAGGGCCCT ATATGTTCTT ACCACATACA GAGGATGCAT 120
TTATTTTTCG TCTATGACAC TTGCAAAAAT CTCTACTGTA ATTAATTTGG GTCTATTATT 180
AACTCTCTGT TCCATCATAG AATGTGGCCA GGCCTTACAA TGGAGAGCCA GAGTTAAAC 240
TTCAAGTTGC ATCTGTTTTT GGGCTGAGTC ACCACCGGAC CTCGAG 286

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCGGCC AAAGAGGCCT AAAAATGAAA ACCTCTGCAC TTTAATTTTT TTCAGTAATT 60
TCCAGCTATT TCTAGGTATA AAGAGCAGCT CGTTCTCTT ATTTATTTTA GTCTCATGTG 120
TCAATACTTT CCGATGCTTT GCTTAATTCA TGTATGTGTG CAGTGCTGCA ATGCCCAGAC 180
AAACGTGAGC ACACCCACCA ATCTCGAG 208

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GAATTCGGCC AAAGAGGCCT ATGATGAAGC TGGGCATTTA TAACTAGATT CATTAAAGGAA 60
TACAAAGAAA ATACTTAAAG GGATCAATAA TGGTGTCTTC TGGTTGCAGA ATGCGAAGTC 120
TGTGGTTTAT CATTGTAATC AGCTTCTTAC CAAATACAGA AGGTTTCAGC AGAGCAGCTT 180
TACCATTGCG GCTGGTGAGG CGAGAATTAT CCTGTGAAGG TTATTCTATA GATCTGCGAT 240
GCCCGGGCAG TGATGTCATC ATGATTGAGA GCGCTAACTA TGGTCGGACG GATGACAAGA 300
TTTGTGATGC TGACCCATTT CAGATGGAGA ATACAGACTG CTACCTCCCC GATGCCTTCA 360
AAATTATGAC TCAAAGGTGC AACAATCGAA CACAGTGTAT AGTAGTTACT GGGTCAGATG 420
TGTTTCCTGA TCCATGTCCT GGAACGCTCG AG 452

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

```

GAATTCGGCC AAAGAGGCCT ATCTTCCTGA AGAGCAATGG AGCCGCTTTT ACTTGAAGA      60
GGACTAATCG TATATCTAAT GTTCCTCCTG TTAATAATTCT CAAAAGCAAT TGAAATACCA      120
TCTTCAGTTC AACAGGTTCC AACAAATCATA AAACAGTCAA AAGTCCAAGT TGCCTTTCCC      180
TTCGATGAGT ATTTTCAAAT TGAATGTGAA GCTAAAGGAA ATCCAGAACC AACATTTTCG      240
TGGACTAAGG ATGGCAACCC TTTTATTTC ACTGACCATC GGATAATTCC ATCGAACAAT      300
TCAGGAACAT TCAGGATTCA CAACTCGAG                                     330

```

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

```

GAATTCGGCC TTCATGGCCT AAGCAAACCC AGAGGTGGAT GTTATGAACA GCTGTGTCTG      60
CCAAACACAT TTACCCCTTG GCCCACTTT GAAGGGCAAG AAATGGCGTC TGCTCTGGTG      120
GCTTAAGTGA GCAGAACAGG TAGTATTACA CCACCGGCC CCTCCCCCA GACTCTTTT      180
TTGAGTGACA GCTTTCTGGG ATGTCACAGT CCAACCAGAA ACACCCCTCT GTCTAGGACT      240
GCAGTGTGGA GTTCACCTTG GAAGGGCGTT CTAGGTAGGA AGAGCCCGCA GGGCCATGCA      300
GACCTCATGC CCAGCTCTCT GACGCTTGTG ACAGTGCCCT TTCCAGTGAA CATTCCCAGC      360
CCAGCCCCAT CCTCGAG                                     377

```

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

```

GAATTCGGCC TTCATGGCCT AGGCAAGGTC TTCGGCTCGT GCCGTTCTAA GCCGGAGAAT      60
TCTCGCGGGA GCAGGGTTAC GTCCTCGTGG GATTCGTTGG CGGTGGCTGA GGTCTCCAG      120
CAGCCTGACC TGAGTGGGTT AGTGATCCAG AGAAACCAGC AGGCCAACTT GGTGAGGAAG      180
GTTTCGGGAAG CTGTTGGAGC AGTGTGGGGA ATTTCCACC AGGATGAGTA TGATTGGCTG      240
TGATTTTAGA TCGTAAAGCT GAAAATTGAA ATCATGAAAG TAGACAGGAC TAACTGAAG      300
AAGAACTCGA G                                     311

```

(2) INFORMATION FOR SEQ ID NO:402:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GCATTGATGG AAAAGCATAA TGTCTTAGAA AAAGGCTTTC TAAAAGAAAA AGAGCAAGAG	60
GCCATTTCTT TTCAAGATAG ATACAAAGAA CTTCAGGAAA AACATAAACA AGAATTGGAA	120
GACATGAGGA AAGCTGGTCA CGAAGCCCTC AGCATTATTG TGGATGAATA TAAGGCACTA	180
CTGCAGTCTT CAGTTAAGCA ACAAGTAGAA GCTATTGAAA AACAGTACAT TTCTGCAATT	240
GAGAAACAGG CACACAAGTG TGAGGAGTTG CTAAATGCTC AGCATCAGAG GCTCCTTGAA	300
GTGCTAGATA CAGAGAAGGA ACTGTAAAAA GAAAAAATAA AGGAAGCCCA TCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:403:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GTTCTAGACC TGCCTCGAGC GTTAATGGTA TAAATCACTT GTTTGTAAAG TATTGTTTTT	60
AAATATTGCC AGATTGATA TCTTAGTATT GTATTTTAT ATTTGTCTTC ATGTGTTTTT	120
GTTTTCTCAT AAGTGTCTGT ACCCCCCTTT TTTTTCTTT AAAGAGAAAT AATGAGAGAG	180
ATTGTCTGTC TTGAAGTTCT CAGTGCCTGT GCATTGCTGC CACTACACAG CTAGTATCAT	240
GACAGCAGCT TCAGAACCAG AGCTGGCTTC CAGGCAAGGC TGGGTGGGGA AGAAAGAGAA	300
AAACAAAAGA ATTATTTCTC TATGCCGAGA CCAGCTCGGT CAGGGAGACC CTAACCTAGC	360
GGTGCTAGAG GAATTAAAGA CATAGACACA GAAATATAGA GGTGTGAAGT GGGAAATCAG	420
GGGTCTCACA GCCTTCAGAG CTCAGCCACG AACAGAGATT TACCCACGTA TTTATTAACA	480
GCAAGACTCG AG	492

(2) INFORMATION FOR SEQ ID NO:404:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 395 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GAATTCGGCC TTCATGGCCT ACTTCCCTCT AAGGTCCCCA AATGCCTCTC ACGTGCCTAG	60
CATTTAGCTG CTGACCGAG CATGCTCACT GACAACTTT TGGCCAAGAA GAGCCTTTTG	120
GTCTCTCTTG GTCAGATCTA GGAGGGCTTC AGGACTCTCC AAAACTCACC CACTCAGAGA	180
GCCTGCCAGG AACACTCAGC TGAGCGATGG CATTGTGGAG CCTGGGTTTT CAGAAGGGAG	240
CCCATAGTGA GTGGTAGCAT AACCTTGTTA AGGTTGTATT TTCCTTAGAT ATAGAAACAA	300
ATCAAATGCT GCTAAATTGG TAAGGGATGG AGTTTTATA TCACGTCACA TTTGCTGAG	360
CCGTAACCAG ACAGGGAAAA AGCAGAGACC TCGAG	395

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

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GAATTCGGCC TTCATGGCCT ACCAAGTTCT AACTGTAAAA TGGGGACATT TTACCTTTCT      60
TTCTTTGGAT AGGATCAGTT CTTAAGAGCA GCCCCGGTAA CTGGAGGAAT GGGAGCCGTT      120
TTGATGAGAA AAATGGGCTG GAGAGAAGGA GAAGGATTAG GAAAAACAA AGAAGGCAAT      180
AAGGAACCCA TCCTAGTTGA TTTAAGACA GACCGAAAAG GTCTTGTTC AGTAGGAGAA      240
AGAGCACAAA AGAGGCCTCG AG                                     262

```

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

```

GAATTCGGCC TTCATGGCCT ACCCATTTGT CAATTTTTC TTTGTTGCAA TTGCTTTTGG      60
TGCCTTTGTC ATGAAACCTT TGCCTACAGG TGCTGTTTAT TTACACCCCT GTCCCAACCT      120
CACCCCACTC CTTTTCTTTT GCTGGTGGGA AGTCAGTAAG AACTGTGGGT GGGGTTCTGA      180
GGTAATCAAT ACAAAGAAGA AGGTAAGAAA TTGGAGGGGA CTCAGGGGAG ATGGCAATGC      240
TGACAAGGGG TTGGATGGAA TTTGTTCTGT AAAC TGGAAG CAGCTCGAG                289

```

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

```

GCTCCTTCTG TATCCTTCCT TTCCCATCTG TCTGCTTCTA ACAAATAAGA CAAGCTAAGA      60
AGCAGCTTGT TTCATGATTC TATACTCACT TCCAAGCTTT CTCTGCATAG ACTTTCCTAG      120
TTTGCCACTT TATCTTTTCT CCATCCCTCC AGCCAGTCAT GAGATTCTAC TCCCCATTCA      180
TACATGCATT TATTATCCA GACTTTACTG AAGGCTTACT CTTTGAACCT TGCAAAATGC      240
CAGTGAGGCA AAGCATGCAT CCTGTACAGG AAAA ACTCAG TCTAGAGGGG AGAGATAAGC      300
AAACAAGTGA TTACCACACC AGGCTCGAG                                     329

```

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

ATTGAATTCT AGACCTGCCT CGAGAGCTTT TGAGATTGTC TATTTTGTCT GAGTGAGTTT	60
TGGTACTTTA TTGTTTTCGA TTGGTCCATT TCTTCTACGT TGTCAGATCT CTGAGTGTCA	120
AGTTGTTTCAT AGTACTCCGT TATTATCTTT TTCATGACTG TAGGATCTGT GGTGATATTG	180
ATGATTTTGTG TCTTCACTCC TTTTGTGTGG CCTACACTCG AG	222

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 505 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GAATTCGGCC TTCATGGCCT AAACCTGCAG AAATGAAGAC TAGAGTACAC AGCACACTCA	60
GAGCCCAGAC AGACTTCGTC CCAGGACATC ATCTGTTCTT GATGCCCATT CTTCTCTCCT	120
AAACATCATT TACTTTTTCC TCTAAAAGTG CCTGCAGACC CCCACTACTC TCTCCCATGG	180
AGAAGGGCAT ATAAGCTTCG AATCTCACGG GGTATTGGG CACTCTGTCT CTTGTGATGC	240
TCCTATGCAT GTAATAAATT TATGTGCCT TTCTCCTATT AATTGGTCTA ATGTCCATTT	300
ATTCCATAGA TTCAATTATC AAACCTCTCAG AGGGCAGAGG GAAAATTTTC ACTCCCTTAT	360
ATCATCAGAA ATATAAATAA AAATAGCACA ACACTCAGTA AATGATTATG TTATTATTGT	420
TATGTTTGTG ATATCTTGGT GTCTGGTTAT TTAAATCAT ATCACTTAAA GAAACAGTGT	480
TCCTTAGGCC ATGAAGGCCG AATTG	505

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

GTATGAACAT TGAGGGCCCA GATCTCAATG TGGAAGGTCC GGAGGGAGGC TTGAAAGGTC	60
CCAAATTCAA GATGCCTGAC ATGAATATCA AAGCTCCCAA GATCTCCATG CCTGACATTG	120
ACTTAAACTT GAAAGGCCCC AAGGTGAAAG GTGATGTGGA TATTTCTCTT CCCAAACTTG	180
AAGGGGATCT GAAAGGGCCA GAGGTGATA TCAAAGGCCC TAAAGTGGAC ATCAATGCCC	240
CAGATGTGGA TGTTTCATGGT CCAGACTGGC ATCTGAAGAT GCCCAAAGTG AAAATGCCCC	300
AGTTCAGCAT GCCTGGCTTC AAAGGAGAAG GCCCTGAAGT CGATGTTACC CTCCTAAAG	360
CTGACATTGA CATTTCCTGGT CCAATGTAG ACGTTGATGT TCCAGACGTG AATATTGAAG	420
GTCCAGATGC AAAGCTGAAG GGCCCAAGT TCAAGATGCC TGAGATGAAC ATCAAAGCCC	480
CCAAGATCTC CATGCCTGAC TTTGACCTGA ACTTGAAGGG ACCCAAATG AAGGGTGATG	540
TGGTTGTGTC TTTGCCCAA GTGGAAGGTG ATCTAAAAGG CCCTGAGGTG GACATCAAGG	600
GCCCCAAAGT GGACATTGAC ACTCCTGACA TTAACATCAA GAGGCTCGAG	650

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

```

GAATTCCGCC TTCATGGCCT AGGGGCTGGA GGGTGGCCCG AAGCAGATGG GGCCGGCCTT      60
GCAGGCACTT CTAAGGCCTT GGGGTTTGCT TCCGAGGGAG TAGGGAAGGA GAGCGATGTC      120
ACCTGTGAG GCTTGGTCAC ATACCCCAAT GGATTTGGTA GCACACGCCA CAGTGAAGGT      180
ATAAGCTACT GTCATCACAC GTAATTATTT CATGAAACAG AAAATTTTAA AATAAAAGAA      240
AATAGAAGTT TCCCTATTTT CTTCTCCTGC ACTATTGGAT CATCCTGTTT AGCCCTCTTT      300
TAAGACAAAT GGAAGTAGCA AACGAGTGTA AATAGGAATG AATGGTTTGT TGGGGTTTAT      360
TTTATTTTAT TTTATTTTAT TTTATTTTAT TTTATTTTAT TTATTGAGAC AGAGTTTCAC      420
TCTGTGTCG CAGGCTGGGC TCGAG                                         445

```

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

```

GCCTGCCTCC AGGCCTTTGC TCCCACTGTT GNCTCCACTT AGAATAACAT TCCACCCCAT      60
CTCTATAAAT ATCCTACAGA CAAATACTAC CTTCCCTTA AGGCCAGTTC TAACCCTAAC      120
TGACAACAAA TCATCTCTAC ATGATCTTTT CTTCTGGGA ATGCCTGCAG CACTGTTTAA      180
TCCTGCCCCA CCACCATCCC CTCACCCAGC ACCCTCTCCC AGACCAGACA GGGTGGCTCA      240
TGCCCTGCAAT CCCAGCACCT TGGGAGGCTG AGGCAGGAGG ATTGCTCGAG      290

```

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

```

GAATTTGACA TCTTAGAACA TTCTGCAACC TTTTGCTGG GAAATGGAAA CAGATCTAAT      60
CTTTACCACC CTCATGGCTC AAGGACCTCA TCTGGCAGCC TGGCTCATGT TTTTCAGCCA      120
AGTAGCTTCC AGCTTACAGC AGCCCTCAAA TTTGGACCTG CCACCAGCTC CAGAGCTTGA      180
CTGGATGGAG ACAGGACCAT CTCTGACATT CATTGGCCAT CAGGATATAC CAGGAGTTGG      240
TAACATCCAC TCAGGTGCCA CACCTCCCTG GATGATCCAA GATGAAGAAT ACATTGCTGG      300
GAACCAAGAA ATAGGACCAT CCTATGAAGA ATTTCTTAAA GAAAAGGAAA AACAGAAGTT      360
GAAAAAATC CCCCAGACC GAGTTGGGGC CAACTTTGAT CACAGCTCCA AGGACCTCGA      420
G                                         421

```

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

```

GAATTCGGCC TTCATGGCCT AAGCCAGTCA ACCAGCAGTA TTAGTGCTGT TTTCAAAGAT      60
TTAAGCTCTA TAAAAATTGGG AAATTATCTA AGATCATTTT CCCTAAGCAT TGACACATAG      120
CTTCATCTGA GGTGAGATAT GGCAGCTGTT TGTATCTGCA CTGTGCTCTG CTACAAAAG      180
TGAAAAATAC AGTGTCTTACT TGAAATTTTA ACTTTGTAAC TGCAAGAATT CCAGTTCAGC      240
CGAGCCACTT CGAG                                         254

```

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

```

GCAAACAGAC AAGGCTTACA GGTTAGTTCA GGATCTGCGC CTTATCAAGC AAATTGTTTT      60
GCCTATCCAA CCTGCGGTGC CAAACCCATA TACTCTCCTA TCCTCAATAC CTCCCTCCAC      120
AACCCCTCCA TAACCCATTA TTCGGTTCTG GATCTCAAAC ATGCTTTCTT TGCTATTCTT      180
TTGCATCCTT CATCCCAGCC TCTCTTTGCT TTCACTTGGG CTGGCCCTGA CACCCATCAG      240
CCTCAGCAAC TTACCTGGGC TGTACTGCCA CAAGCCTTCA CGGACAGCCC CCATTACTTC      300
AGTAGCCCTC GAG                                         313

```

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

```

GCCTGCCCCC ACCTTACAGG TCTGGGATGT ACCTTTCCAT CTGTTGCTGC TTTCTTCTAT      60
GGGCCCCTGC CCTCACTCTC AAGAACCTCA ACTACTCCGT GCCGGAGGAG CAAGGGGGCCG      120
GCACGGTGAT CGGGAACATC GGCAGGGATG CTCGACTGCA GCCTGGGGCTT CCGCCTGCAG      180
AGCGCGGCGG CGGAGGGCGC AGCAAGTCGG GTAGCTACCG GGTGCTGGAG AACTCCGCAC      240
CGCACCTGCT GGACGTGGAC GCAGACAGCG GGCTCCTCTA CACCAAGCAG CGCATCGACC      300
CGGAGTCCCT GTGCCGCAC AATGCCAAGT GCCAGCTGTC CCTCGAG                                         347

```

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

```

GAATTCGGCC TTCATGGCCT AGCAGATGAT TGACATTGCT ATCGATGGTT TCCTTTTGAC      60
TCCAGTGCAG AAGATCTGCA AGTATCCCTT ACAGTTGGCT GAGCTCCTAA AGTATACTGC      120
CCAAGACCAC AGTGACTACA GGTATGTGGC AGCTGCTTTG GCTGTCATGA GAAATGTGAC      180
TCAGCAGATC AACGAACGCA AGCGACGTTT AGAGAATATT GACAAGATTG CTCAGTGGCA      240
GGCTTCTGTC CTAGACTGGG AGGGCGAGGA CATCCTAGAC AGGAGCTCGG AGCTGATCTA      300
CACTGGGGAG ATGGCCTGGA TCTACCAGCC CTACGGCCGC AACCAGCAGC GGGTCTTCTT      360
CCTGTTTGAC CACCAGATGG TCCTCTGCAA GAAGGACCTA ATCCGGAGAG ACATCCTGTA      420
CTACAAAGGC CGCATTGACA TGGATGCTCG AG                                     452

```

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

```

GATAACTTGA GATCAAATCA GTCATATTTG ACTCTTCTCT TTTTCACTCC TTTTATATCT      60
GATCAGTCAG CAGTTTTTTG AAACCCCTGT CGAAGCAGTT CTCAACACTT GTGCACCCAT      120
TCTTTCTCCT ACACCACTCA ATCTAGACCC TCACATGTGG CTGTCCTGCT TTCCTTCTCT      180
CCTACTTCTA AGCTATTCTG TGGAGAGATG TCAAAGTAAT CTTCAAAAA AATCTGATTG      240
CATCACTTCA CATCTCGAG                                     259

```

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

GAATTCGGCC AAAGAGGCCT AATTAGAAAT GGCTACTCCC CAGTCAATTT TCATCTTTGC      60
AATCTGCATT TTAATGATAA CAGAATTAAT TCTGGCCTCA AAAAGCTACT ATGATATCTT      120
AGGTGTGCCA AAATCGGCAT CAGAGCGCCA AATCAAGAAG GCCTTTCACA AGTTGGCCAT      180
GAAGTACCAC CCTGACAAAA ATAAGAGCCC AGATGCTGAA GCAAAATTCA GAGAGATTGC      240
AGAAGCATAT GAAACACTCT CAGATGCTAA TAGACGAAAA GAGTATGATA CACTTGGACA      300
CAGTGCTTTT ACTAGTGGTA ACGGGCTCGA G                                     331

```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GAATTCGGCC AAAGAGGCCT AAGAGCATTT ACCTGTCCTGA CAATTGTATT TTTAATGATA	60
GTTTGCTTTT ACTTGGTCTT TATATATTCA ATTACAAATT ACTGATATTT TGTTTAAATC	120
TACCACATTT TTCCATTGA CTGTTTATTT TTATGTCCTT TCTTTCTTTT AGATTAAGTC	180
TTTTTCTTC TCACCCCTC ACCCTCCCC CCTGTTATA CATTCTTTTA CTATTCTTTT	240
TGTTATTCCA TAGTTGCAGC AACTCGAG	269

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GAATTCGGCC AAAGAGGCCT ACATTGAGGT AAGAGATATT TAAAAGGTTT TTAGGTGAAA	60
TTTGAAGCAG GGTAGAGATT GGGATTCCAC CTTTGTGTC ATGCATACCT GTTGATAATC	120
AGCTGTTTCT GTATCGACTC CGTGTCAACT CCAGAGCAGG GGGTATCCTC CTGTAGTGCA	180
CCTTCTCTCT TGGCCTGGAG GCAGCACTTT CTGTGCCTGG GCAGCAGAAA TGGGGAATGT	240
TCTTTGGTCC GTTGAAAAA CGGGCCCAA CATCTAGCCC TGTGCATAA GGCATGGAAT	300
TGCCCAGTTG GGGAGGACCT GTGCTGGAAA GGGATCATCA AACTCCATCT GCCCATCAG	360
ATGCCTGAAC TCTTGATACA ACTCTGCCA TCCAAGCTAC TCGAG	405

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 327 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GAATTCGGCC AAAGAGGCCT ACTCGTACTT ATTTATAAAA AAAGTAACT GTAAAACAGC	60
CTCAGGCAGG TCCTTCAGGA GGTACTCCAG AAGAAAGTAC TGTTATCATA GATGACAACT	120
CCATATGTGT TATTGCACCT GAAGACCTTT CACCTGGACA AGATGCCGAG GTGGAAGACA	180
GTGATACAGA TGATCCTGAG TATCTTAGTT TTTTGTGTTT TGTTGAGACG AAATCTCACT	240
CTTGCCCCCA GGCTGGAGTG CAATGGCAG ACCTCGGCTC ACTGCAACCT CTGCCTCCCG	300
GGTCAAGCG ACTCTCCAAG CCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 315 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

```
GAATTCGGCC AAAGAGGCCT AGAATAATAC ACTAGTAAAA AAAAATGTAT GTCAGGCACT    60
GGGAAGGCCA GTAGGAATAT AGAAATGAGA AGCCGTGGAT TAGAGACTCA CAGTCTACTG    120
GGTAAAAGAA TACGAAAGCC AATGTATTAT ACTGTGGTAG CTGCTTTAGT AGATGTATGG    180
ATAGAAAAGT AACAAGAGAA GAGAATGACT ATCTCTGCCT AACAGAAAGA TATTTTAAAA    240
GAAGGGTTTT GGGGCTGGAT TTTGAAGGCT CAATAGGCTC CTACCATATA GAGAACTAGG    300
AAGCGAGTCC TCGAG                                     315
```

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

```
GAATTCGGCC AAAGAGGCCT ACTATCCAGG TTTACATTTT AAGGCAGTCG AGACCTTATT    60
CACGTGGTAT ATAAACAACC ACATTTCTCT TTTATATGGA ACAACACTTT TCATTTGCGG    120
CTGGCCTTCT CACTAGCTTA TGCTTTTTTT TTTAAGACC TTTCTTAGCA CTCGCTGAAC    180
TCCTCCCCCT CACAATCAAT CTCAGCAACT CAGCAGAGTC GCTTCAGTTC ACAGCTCTTA    240
ATCCTTCACT CCAGACTAAA GCTAATCTTA TGTCTCAA CAGCTACAAC TCACTGTTAT    300
CACAGTTCCG ACAGCAGAGA CTCGAG                                     326
```

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

```
GAATTCGCCA AAGAGCCTAT AGAAATAATA CCACGACCTG CGCATTCAAA GCTGTTGTAT    60
CTGGATTGTG ACTGCGTGGA AGGTCGAGGC GGAAGACAG GGGCTGTTGC TTTTCGTTAT    120
AAACTCTGCA TTAATTGATT TTTGCACTAC GTACATTAC TTTGATAACA CTGGAAAGAA    180
TAAATTGGCC ATGTAGTGTA GCTTCCAAAA AAAACTATTG CTTGGGTTTC AAGGTCAAGG    240
AAATTTTCATT CTCATCAGTT TCTTGGGAAA GAGGAAGTGG AATGATGTTG TCAGAAAGTG    300
AAACCATGGG TCATTTTCAG AACTACTCAG AGTAATAAAT ATTTTTGTC AGTTTGTTC    360
TTACAAGTGA AATGGTCCCC TCGAG                                     385
```

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 460 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GAATTCGGCC	AAAGAGGCCT	AAGAGATTTT	TATTATGATT	TTGATTTCCT	TACTACAACA	60
TTGCATGTGT	CTGGAGTATA	GCCATTACAC	TTTATGAAAA	AGGCAAAATG	GTCATTTGGG	120
GTGTTT TAGG	AAGTTTGCCA	AAAGGCTCCT	TTGTCATTAT	AATCCTTCCT	AAGCTGCCAT	180
CCACGGGTTT	AGGTCATGGA	TATGAAAAGT	GAAAGGGTTT	AGAGATGAAG	TAGTGTCCTC	240
TGAGTGCTTA	CCAACCTGTT	AATCTTTTGG	AGATGTTAAT	TTTTTCATAT	AGAGCCCCCT	300
AAAATCTTGA	TGGCTCTAGA	TCAGTCAAGC	CTAAGAGAAG	ACGTATTTAT	GGAAAAAAC	360
AAAAAACAAA	AAAACCTTGC	TGGATTGCTA	GTAATATCTA	CTTCTTGGA	ATTAATACTT	420
CATATTTTTT	AAAAAATTA	TTGATGCATT	AGGACTCGAG			460

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GAATTCGGCC	AAAGNGGCCT	AGGAAAAACA	TGAAATACAT	AAATGGATTA	ATTTTGCAAA	60
TTAATCTNGC	AAATTAATCT	ATAGCTCTTA	ATGTTTCTTC	CAAATTAAAG	GAAAAATGGA	120
TAAGGAAGTA	CTTCTTGGC	AACTGTAGA	TGAATACTGA	ATAAAAGTCA	TTCTTTCCTA	180
AAGAAGAAAA	GTGCATTTTA	GTTTTTTAGA	AAAAATGTAA	TTTTAGAAAG	TCTCTTCTAT	240
GCAGATTTTA	GAAAGTCTTT	TCTATTTTGA	GAAAGTCTTC	TTGTATGCAG	ATTTTGTTCA	300
ACTTCCCCAT	CTGTACTTAC	CAAAGGAAAA	ATAAACAGTT	TATAGAATAT	TAATAGAATA	360
ATTATGTGCN	ATGTAAAATA	TGTTGAATCT	CCCTAATTTA	TATTTACTAT	GTGAATATAA	420
ACTACAGAAT	AAAGAACTG	TTCCTCCTTT	TATCCATTAT	TTTGTTGAAA	ACAACATAAG	480
AAATCTTACA	GATTAATGTT	CATATTAAAA	GGACTCCTCG	AG		522

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GAATTCGGCC	AAAGAGGCCT	AGGTAGTTAT	CAAGAGATTT	TAAAACTTCA	ACCCTTTTTC	60
TCTTATAGTT	AGTGAAGAGA	GTAAGAATATC	TCCAGTTTGG	GCTGACATCT	CTACAACCTG	120
AACAATTGGC	TTAAACTTCA	CTTGGGATTG	CCGTTTGCTT	GTTT TAGCAT	GGCNAAATTT	180
GGCGTTTACA	GAATCCTTCT	TCTGGCTATT	TCTCTGACAA	AGTGTCTGGA	GAGTACAAAA	240
CTGCTGGCAG	ACCTTAAAAA	ATGTGGTGAC	TTGGAATGTG	AAGCTTTAAT	AAACAGAGTC	300
TCAGCCATGA	GAGATTATAG	AGGACCTGAC	TGCCGATACC	TGAACCTCAC	TAAGGGAGAA	360
GAGATATCTG	TTTATGTTAA	ACTTGCAGGA	GAAAGGGAAG	ATTTGTGGGC	AGGAAGTAAA	420
GGAAAGGAGT	TTGGATATTT	TCCCAGAGAT	GCAGTCCAGA	TTGAAGAGGT	GTTTCATATCT	480
GAGGAAATTC	AGATGTCAAC	GAAAGAATCT	GACTTTCTTT	GTCTTCTTGG	AGTAAGTTAC	540
ACATTTGACA	ATGAAGATAG	TGAATTAAAC	GGTGAACCTG	AG		582

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

```

GAATTCGGCC AAAGAGGCCT ACTGATCAAG TGACCCATTA CTGCGGGAAA AAACCACACA      60
TACAAAAGCC TTGACCCCA GTAATTTGT ATTGGTATAT TTACCCTGAT CTTAAACTGC      120
AAGGAATGTC CGCAATTAGA GTTTTCTTT GTTTTCTAAG TCTGAACTT GATAATCCAT      180
TTCTGCCTTC CCATGACGAG TGGACATTCC TCCAGCCAGT GGTGAGTTCC TCTTTCCTTC      240
GCTCTCAGCA AGAGCATGGG TTGCCCTCCC ATCTCGTAAG CAGAGCCTAC CACAAACGCA      300
GCTCAAATCT CGAG                                     314

```

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

```

GAATTCGGCC AAAGAGGCCT ATTGGGTCCT ATTTACAAC TTAAGAATGG AGGCATACTT      60
CAGGAAAGAA AGCACCAGTG CAGTTCCAAT TTATTATTGT ATCTGCTGTC TTGAGAGTAC      120
AGGGTGTATG AGAGTGCACA GTGGTTTAGA ATCACTATGG AATT'TAAAAA GACCCAGAGA      180
CATTAAACAAG AATCCACATT CTAAGTCGTC AGAATCCACA TTTCTGACCT TGTCTGCTGG      240
GGCCTGCTCT GTTTTGTATG GCTCAAAATA TAATCTTTT ATTGAAATAC ATGTTCTCTCA      300
TCCTGTTTCA GGGCTTCTGC CTGGAATGTT CCTCCCCCTA GCATTTGTAG GGCTGGCTCC      360
TTCCTGTCTAT GCAGGTCTCA GCTCAGATGA CCCCATCTCA GAGAGGGCTT CCCTGACCAA      420
CCAATCTACA GCCCTTCCTA GTCACTTTTT TCCACATCAC CCTCTTTATG CATGGAGGCA      480
GATAGGTGTT TTACCCTGTT TATTATTAT TATTATTTT TTGAGACAAA GTCTTGCTCT      540
GGCACCCAGG CTCGAG                                     556

```

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

```

GAATTCGGCC AAAGAGGCCT AGAAGTAACG GAAGCTACCT TGTATAAAGA CCTCAACACT      60
GCTGACCATG ATCAGCGCAG CCTGGAGCAT CTCCTCATC GGGACTAAAA TTGGGCTGTT      120
CCTTCAAGTA GCACCTCTAT CAGTTATGGC TAAATCCTGT CCATCTGTGT GTCGCTGCGA      180
TGCGGGTTTC ATTTACTGTA ATGATCGCTT TCTGACATCC ATTCCAACAG GAATACCAGA      240
GGATGCTACA ACTCTCTACC TTCAGAACAA CCAAATAAAT AATGCTGGGA TTCCTTCAGA      300
TTTGAAAAAC TTGCTGAAAG TAGAAAGAAT ATACCTATAC CACAACAGT TAGATGAATT      360
TCCTACCAAC CTCCCAAAGT ATGTAAAAGA GTTACATTG CAAGAAAATA ACATAAGGCT      420

```

CGAG

424

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

```

GAATTCGGCC TAAGNGGCCT ACATAAAAGT AAGAAAATAT CTTACTAAAA TCTCTTTTCT      60
TATAACATTT AGNTTACGTA TATATTTTAT CTCCCTTTTT TTGNAATATA TATAAATCAA      120
ATAACAGCTG AATAAACCTT TGGTCTTTTT TTTTTTTTTT TGTCTCAGGA TTGTCTTTAT      180
CTGGGACCCG AGATTAATTG CTTCGTTTTT GCTTTGGCAA AAGATTGTTT TTACAATTTT      240
TAGTCTTTTA AAGTTGACAC AGATTGTGTC AGTCTTGCTC ATTCTAAAAG CACACAAAAG      300
TTGAGCATAA AAATAGGATT AAATTTAGCA ATAAAGAATT ATAAAGACTA AAAGATACTG      360
AGTAAGTTGT TTGACAGAAA CCTGATTATC CATGATGATT ATTTGCAGGC TTCTCGAG      418

```

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

```

GAATTCGGCC AAAGAGGCCT AGAACTCCAG AGGCAAGTGT TATATGAATT ATGCATTTGA      60
TTCTACATGT TTATTAGACA TGTATGCGAG ATACATTATAT ATTTTACTAA TGGTTATGAT      120
GACTTTAATA ACTTTCAAAG GATTATGGGG ACTCGAG                                157

```

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

```

GAATTCGGCC AAAGAGGCCT ATGTTTTTAC TACTATTATT TTTTTTTACC CAAGGGAGAA      60
AGACAAAAAA ACGGTGGGAT TTATTTAACA TGATCTTGGC AAACGTCCTC TGCCTCTTCT      120
TCTTTCTAGA CGAGACCCTC CGCTCTTTGG CCAGCCCTTC CTCCCTGCAG GGCCCCGAGC      180
TCCACGGCTG GCGCCCCCA GTGGACTGTG TCCGGGCCAA TGAGCTGTGT GCCGCCGAAT      240
CCAACTGCAG CTCTCGCTAC CGCACTCTGC GGCAGTGCCCT GGCAGGCCGC GACCGCAACA      300
CCATGCTGGC CAACAAGGAG TGCCAGGCGG CCTTGGAGGT CTTGCAGGAG AGCCCGCTGT      360
ACGACTGCCG CTGCAAGCGG GGCATGAAGA AGGAGCTGCA GTGTCTGCAG ATCTACTGGA      420
GCATCCACCT GGGTCTCGAG                                440

```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

```

GAATTCGGCC AAAGAGGCAT AACATAGAG AAATTGGTGA TGTTAAACCT TCTGAATTTT    60
GTTTTAAGTG CACTGGGAAG TGATGGAAGG GTTTGTAGCA TAGCAGTAAT CTGATCTGAT    120
CTGATCCGGT GTGAATGTCT TTTTAGCAGA TGATTTTCATT TTACCAGCTC TCTNGAAAGT    180
TTAATCAATG TGATAGCCAT GACAGTTTAT TAAACTACTT ATTTGAGAAA GTAAGTGCCT    240
GTGGGAATCC AGATTATTTG TTTACTTCAT TTTAGATGTT AGTGCTAGCA CCCTTGTTTA    300
ATATTTGTTT TAACACTTAT ATACTTAAAA GCAGGAAATC TCGAG                    345

```

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

```

GAATTCGGCC AAAGAGGCCT AAGAACTCAC AATAAAGTAT CATATTCCTC TCTTTTGACC    60
TAGAATTCAT AGCCCTAGTA ATCTCGTTTT GATTAGATGC TTTGATTGGC AGTTATACAT    120
CTTTGATAAC ATTTTCAATG TGAAATGAAT TATCTTTTCG TTAAAGCCAT TTAAGCAGA    180
ATGTCTATAA ATGAGGGCCC ACGAGAAGGA ATAACAAAGC AGGGGTGTTG GGGATGGTGG    240
CTGGGGAGCT TTGGTGTATT TATTAACCTG TGGTTGAGTT TTGCGATGTG TGCAAGTACA    300
CACAGCCCCG AACAACTCGA G                                         321

```

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

```

GAATTCGGCC AAAGAGGCCT AGTTTAAAAA CGTATTGTTT AATTTTCNAA CATTTAGGGA    60
TTTCCCAGAT ATCTTNGTTG TNGGTTTCTA ATTTGATTCC ATTATGGTTA GAGACCATAC    120
TTGGTATGAT GAATTAAAAA AAAAAATNTA GAGGTTTGTA TATGGCCTGA AACATTTTTT    180
AGGTGAGTGT TCAGTTTGTA ATAGGAAAGA TGTGTCCTGC TGCCGTTAGG TAAAGTGTTT    240
CATAAGTAAT AATTAGGTCA AGTTGGTTGA TCGTGNTAAG GTCTGCTCTA TCCTTGCTGA    300
TTTCTGTCT GCTTGTTCTA GTGATTACTG AGAAAGGAGT GTTGAAGTCN ACAACGATTG    360
TTATGGGTTT GTTCTCTTTC TCCNTGAAAT TCTGTCTGNN TATGCGTCCT GTATTTTGAG    420
GACCCCTCGA G                                         431

```

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

GAATTCGGGC TTCATGGCAT ANGCAAGGT TCCGGGNCCA GNNCANGCNC GGGACAAGNT      60
CAGAGATGAN GTTCCCCANA GTNATGNNGA ACTCCAGTNC CCGNTGTCCC CGNNTTTTCT      120
CTCTTGTGGN ACATGGGGAN NTNTGGANTC CAGCTCCCAG NACTGGAGTG CTATTCAANT      180
GATCNAGGAN GGAAGTGACA NAAATGTTTT TTTTTTTNTT TTTTAAAAAA GNAGNNNCNN      240
GGGGATCNGA AGNAGATGAA TGCCCTCAAA GGCCATGNAT GTACTTCAAA NGAAGTGGNT      300
NNTGAAAACA GNTNNAANAA TGTAANCGA NAGTNAAAAT NNATGTTGNG GANGAAGGAA      360
NTTGGTGGNN AGTNAAAAAA GAAGTAANCC GA                                     392

```

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```

GAATTCGGCC TTCATGGCCT AGGTGTGCTT CCCTTTCCCC ATTTCCCATT ATTCCCAGCT      60
GTATAGTAGT GTAGTGAAAA TCACTTGAGA TGTGGAAGAG TAGTCTGGTC TAGGAAGAGA      120
GAGGGAAGAG TAAGTTTCCC AGGATAAGAG GGGGAAAAAA GGCCCCAAAG CTTTCTCAAT      180
GAGGAATGGG GAAGGAGGTT TTGTGCCAG GTTTTACTAA GTGCATTGTA ATGAACCCTG      240
CTATTGTAGT CCTCTTTTAT TAATGCTTTC CTGACATTTA CCCTGTTAGT TGAGGCTACT      300
CGAG                                     304

```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 579 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

GAATTCGGCC TTCATGGCCT AATCACNGNA GTGACTGACA TTATATATTA NGGATCAAAT      60
TATGTCCACA AGCAATATTA TATAATCTAC GTAGAAGTGT AATAACAAAC AAGAGTACAC      120
TTAAATTTAC TTTAAAGAT GTCTTTAGTT CATTCCAATA TAATCTTGA TTAATTTAG      180
GATTATTTCT ACATTTTAGG ANNTACAAAG GATCACGGGT AACATGGATT GGGNCCANAT      240
ATTTTTTTAA AGTTTCGAAT TGGTATCTGT AGTAGTGGAA TGTTATAGAT TTGAAGTAAC      300
TCTCCACGGA CAGTGCTGCT TTCGTGTAGA GCAATTTAAT TGGAGAAGTG GCCATTCTTA      360
CTTCAGGGAT GCAAAGATGG TCTCATACCA TTTGGATAAA TGTCGTGGTA TCCATGCTTT      420
TTTTCAACTA ATAACATCAT CTCTCTTCAT GACCAGTTAA TTGGGCTATT TGGCAGCCCA      480

```


GTGAACCTAT GTACTAATGG CAAGTTAGGG GCAAATGGAA ATGGACACAT CCGATAAAGT 540
 TGAAATGTAT GTTTTAATCT TTCACAGAAG TCCCTCGAG 579

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 556 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GAATTCGGCC TTTATGGCCT ACCTACGGTA CCTGAAAACA ACGATGGCAT GGAAAACACC 60
 TCCCATTTAC CTGTTGTTGC TGCTGTCTGT TTTCGTGATT CACCAAGTTT CNTCTCAAGA 120
 TTTATCNNCC TGTGCAGGGA GATGTGGGGA AGGGTATTCT ANAGATGCCA CCTGCAACTG 180
 TGATTATAAC TGTAACACT ACATGGAGTG CTGCCCTGAT TTCAAGAGAG TCTGCACTGC 240
 GGAGCTTTCC TGTAAAGGCC GCTGCTTTGA GTCCTTCGAG AGAGGGAGGG AGTGTGACTG 300
 CGACGCCCAA TGTAAAGAGT ATGACAAAGTG CTGTCCCGAT TATGAGAGTT TCTGTGCAGA 360
 AGTAAAGAT AACAGAAGA ACAGAACTAA AAAGATACCT ACCCCCAAAC CACCAGTTGT 420
 AGATGAAGCT GGAAGTGGAT TGGACAATGG TGACTTCAAG GTCACAATC CTGACACGTC 480
 TACCACCCAA CACAATAAAG TCAGCACATC TCCCAAGATC ACNACAGCAA AACCAATAAA 540
 TCCAGGACC CTCGAG 556

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GAATTCGGCC TTCATGGCCT ATTATTTTGG CACCAGCGTC AAGACAAATA ATATCCTCTC 60
 CCATTATTTT CATAAGTAAC ACAGATTCCT TGATTTTTAA AACTAAAAA TACAGCTAAA 120
 CCTTCTTAT GTATAAAGTA TGCCTATCAT ATACAGGGAG AGGTGGGTAA TAACTTCCT 180
 GTAATGACAG TGTTTGGCAT TTCTTTATGG ATGGAATTGG AACATGAACA AGACCATGTC 240
 CAGCGTTTTT ACTGTGAATG TAAATGGAAC AGCAGCCCAA AGCTGTTGTC TGTGCCCCAG 300
 AGGTGCTACC TGTAAGACAG GACCAACTCC ATGTGTGTGT GTTAAGTGTT TGAATCCAAT 360
 TAAGACTCCC AAGCAAATCC TGCATATTC AAATGTAAAG AGTACTCAGT GGGAAAAAGG 420
 TTGTTACCTC AAAGTCATTG CTTCTTTCCT GGCTGGGTCA CAGGGTGAAG AGATGAAGGT 480
 GTCTGATGTA TATAGACAAT TAGGGAAAAA TGAGCGGCTT TCCTCGAG 528

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GAATTCGGCC	TTCATGGCCT	ACTGGAATCT	GCAGCCCCCA	CATGCATCTG	TCTAACGCAT	60
GCCTCGTGT	CGTTTTGCAA	ACATGCCTGT	GGTGGAGGGT	GGTCAGTTGT	AGCCCTGTGC	120
GTCTCAAGGC	TGCCTTGTGA	GGCCATTCCC	AGTGCCTGCC	CTTGAGCTCC	TTACCACCCC	180
TTTTCTGCT	CGGCCCTTTA	ATCCCTGACA	GACCTGGACT	GTGTGGCTGA	AGGGGGACCT	240
GCAGCACTGC	AGAAATGCCT	CTGCGTGGTG	CCATGAAGGA	AAGAAACCTT	GGCCTGGTCT	300
CGAG						304

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GAATTCGGCC	TTCATGGCCT	AGGGCAGGGG	GAGGGGTGCA	NAGTGGGACC	CTCACCACAG	60
GGTACTGAGA	CAGGTCATTG	TAGGTCCGCC	CCGCAATGGT	GTTGAGTTGC	ATCAAGTACT	120
CGAAGTTGGA	TATCTCAGC	TGTACCCATT	TCTGGGTAAG	GCCTGAGGCA	CGCACCATCT	180
CCTGGGGGGA	GCGGCTGCTT	AGGTAGCCAA	GAGAGGGGGG	CCGTAGGCGC	AGGANCCACG	240
AGTACACCTG	GCCCCATCCC	ACCCCATCCC	TCGAG			275

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GAATTCGGCC	TTCATGGCCT	AACCAGCTTT	AATTTCAATT	GAGGAATAAT	AACAACCCTA	60
GAGATTGATA	GGAAAGAGCA	TGAAATACA	TTTTTTGCAT	AAAGATACCT	AAAACCATCT	120
ACCCAGCTTA	GGGTTGAACT	GAATTTCTGT	GAAATAAATT	TGTTTTAAAT	ACTAATTATT	180
TTAAAACTAC	TTAATTCCTA	AAAACAATGT	CATCAGTTTC	AAAAGTTTCA	CTTGGGAGG	240
ATATTCCTTA	AAAGGCATAC	ATAGATGGTA	AAGTATAAAA	TATTTCTGAC	AGAATTATTC	300
AGTATTATTC	AACATTTACT	TTCATGTTTG	TTATTGTACC	ACAAAGATAG	TGTCATTGTT	360
GGTTAAAAAT	GTTGGCTGTT	TTGTTAATA	TACTTAAAC	TGTAACCACT	GGCTCGAG	418

(2) INFORMATION FOR SEQ ID NO:446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GAATTCGGCC	TTCATGGCCT	ACTACATCAA	GCACCAGAAC	CGCCAGCTGC	GCGCCCTGTT	60
GCTCAGCCAC	CAGTTCAAGC	GCCGGGAGGC	CGACCAGACC	CACGCACAGA	ACTTCTCCTC	120

CGCCGTGAAG	TCCCCGGTCC	AGGTCATCCT	GCTCCGTGCC	CTCGCCTTCC	TGGCNTGCGC	180
CTTCCTACTG	ACCACCGCGC	TGTATGGGGC	CAGCGGACAC	TTGCCCCCAG	GCACCACTGT	240
GCCCCTGGCC	CTGCCACCTG	GTGGCAATGG	CTCAGCCACA	CCTGACAAATG	GCACCAGGCT	300
CGAG						304

(2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GAATTCGGCC	TTCATGGCCT	ACAGAGATGG	ATTATCCTAC	TTTACTTTTG	GCTCTTCTTC	60
ATGTATACAG	AGCTCTATGT	GAAGAGGTGC	TTTGGCATAC	ATCAGTTCCC	TTTGCCGAGA	120
ACATGTCTCT	AGAATGTGTG	TATCCATCAA	TGGGCATCTT	AACACAGGTG	GAGTGGTTCA	180
AGATCGGGAC	CCAGCAGGAT	TCCATAGCCA	TTTTCAGCCC	TACTCATGGC	ATGGTCATAA	240
GGAAGCCCTA	TGCTGAGAGG	GTTTACTTTT	TGAATTCAAC	GATGGCTTCC	AATAACATGA	300
CTCTTTTCTT	TCGGAATGCC	TCTGAAGATG	ATGTTGGCTA	CTATTCCTGC	TCTCTTTACA	360
CTTACCCATG	GGAAGTCGAG					380

(2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GAATTCGGCC	AAAGAGGCCT	AAACAAATGA	GGTAGTAAT	TTTTTATCTG	CTAAAACTTA	60
TATTTATATC	ACATACTTGT	TGCAATGATT	TCAGTGTCTA	CATAAATGGT	GGCTTAGCTG	120
AGGCAGGTCT	AGAATTCAAT	CGAG				144

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

GAATTCGGCC	AAAGAGGCCT	ACTAGACGTT	TGTACAAACT	ATTCCCTTGA	GTTATTTTCT	60
CTGGCTCTTC	AGCTCCTTCC	TCCCACCCCC	TCCCCTGCAC	CACCAATCCA	TTCTTTTGCT	120
TAATTTCTCT	CCATCCTTCA	GGTTTCAGCT	TTAAGAGGTC	ACTTCTTTTA	GGAGACATTC	180
CCTGAATCCT	CTCACCTCCA	CCCACAAAAA	AGGCCTCTCC	AGATGCCCTT	CTTTTCTGCT	240
CAAACCTCAT	CTGCTTCCTT	TATCATATGC	TTATCGTTTT	GGATTGTAAT	TATTTATTTA	300
ATTGCATGTC	TTTCTGCTAG	TTTTTGTTT	AGCAACAACA	AGGATCTCGA	G	351

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 505 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

```

GAATTCGGCC AAAGAGGCCT AGATGATGGC AGGAATGAAA ATCCAGCTTG TATGCATGCT      60
ACTCTGGCTT TTCAGTCCTT GGAGTCTGTG CTCAGATTCA GAAGAGGAAA TGAAAGCATT      120
AGAAGCAGAT TTCTTGACCA ATATGCATAC ATCAAAGATT AGTAAAGCAC ATGTTCCCTC      180
TTGGAAGATG ACTCTGCTAA ATGTTTGCGT TCTTGTAAT AATTTGAACA GCCCAGCTGA      240
GGAACAGGA  GAAGTTCATG AAGAGGAGCT TGTTGCAAGA AGGAAACTTC CTACTGCTTT      300
AGATGGCTTT AGCTTGGAAG CAATGTTGAC AATATACCAG CTCCACAAAA TCTGTCACAG      360
CAGGGCTTTT CAACACTGGG AGTTAATCCA GGAAGATATT CTTGATACTG GAAATGACAA      420
AAATGGAAAG GAAGAAGTCA TAAAGACAAA AATTCCTTAT ATTCTGAAAC GGCAGCTGTA      480
TGAGAATAAA CCCAGAAGTC TCGAG                                     505

```

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

```

GAATTCGGCC AAAGAGGCCT AGTCGTAAGT TACCATAATA GGTGCTTGCA GTCATTGATA      60
TAATCCAGAA AGCTAACGAA ATGCAAATGA TCAGGCTCAG TATAACTATA TTAGTTATCA      120
TCTTTATATA TCTTTTGCAT ATATTGTCGT TAAGATCTGT CATGGAAAAT AAGGATATGA      180
GCTCCTGCGG GAAAGAATAT TTAGCGTTTC GGAGAGAAAG TCATTTACGA TGTGAGCAAG      240
ACACTTGTTT AGAGGCAAAC ATAAATCCCA ACATATTCCA CCGACCAAAC AAGCATAAAA      300
ATCACAAAAA TTCAACTCC TTCCGGAAAC TCCTACTGGC CCTCGAG                                     347

```

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

```

GAATTCGGCC AAAGAGGCCT ATCTTACTAT TTTTATGTCA TTGGTTTTTT CTCTTTTCTT      60
TCTTTCTTTT TTTTTTTTTT TTTTGAGGC AGAGTCTCGC TCTGTGGGGA CACTGTTCCG      120
TTCAGAGGCC CCTCCAGCC ATGGGGTGGG GGACAGTGGT GGGCGTGGGA ATCCCAGCGA      180
GCATCCTGGA GGGTGCGTCG TCTCCATGTA TTTTGCTCTT CCCCATCTTT TCCATGGGGT      240
CCCTGCCAG GGTCAAGCAC TAATATGTGG TGAAGGCAGC AAACAGCGTC GGCCTCCCTT      300
TAGGGGTGGG GAGAGGGCTG TAGCACCAAG AACCCTCTCC CCCGCCACG ACATCCCTGA      360

```

AAAGGAGACT AAAATAAAGC CCCGGCGCCT CGAG

394

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GAATTCGGCC AAAGAGGCCT AGGAAAAACA GAGTAAAAA TTGCAAAAGA AGAAGGAAAC	60
AATAACAGAG TCAGCTGGTC GACAACAGAA AAAGAAAATA GAGAGACAAG AAGAGAAACT	120
GAAGAATAAC AACAGAGAT TATCAATGGT TCGAATGAAA TCCATGTTTG CTATTGGCTT	180
TTGTTTTACT GCCCTAATGG GAATGTTCAA TTCCATATTT GATGGTAGAG TGGTGGCAAA	240
GCTTCCTTTT ACCCTCTTT CTTACATCCA AGGACTGTCT CATCGAAATC TGCTGGGAGA	300
TGACACCACA GACTGTTCCC TCGAG	325

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GAATTCGGCC AAAGAGGCCN AGGGTCACAG GGTGTTATC TCACTTCGCA GCTTTTCTT	60
TCTGAGGCCA GAAAAGGAAG GGGTTTGCTT TCCTCTAGTA TTTATTCTTC TGGACTACAT	120
CAAGTACTCT AAGCCTGATG TTAGGCAATA ACTGCCCAT AGCCATTGGC TACATTGGCC	180
TCTTTCTTGT TCCAACAATA TTAGTGATCT GTGGNACAGG ACACACTCTT TGTTTGCTAG	240
CTACAAATTC TAACAAAGCT AAGTTTATT CATGTAGNTA TTCACAAATT AANACACAC	300
ACACACCACA CACACACACA CACACACACA CACACACATA CCACAAAACC	360
CAGAGATCAC CAAATACTAT ATAAATAAAC AAGCCCAAAG TCACAGATCA GGGACACTCG	420
AG	422

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GAATTCGGCC AAAGAGGCCT AGACGTCCAA GAAAAACAT TTGGTGAAAG TCAGGATTTA	60
CCTTTGAAAT CCGACTTGGG CACCAGGGAA GATAGTAGTG TTGCATCTAG TGATAGGAGT	120
AGTGTGGAGC GAGAAGTGGC AGAACACCTA GCAAAAGGCT TCTGGAGTGA CATTGGCAGC	180
ACGGACACTC CTTGCCAAT GCAGTTATCA CCTGCTGTGG CCAAAGATGG CTCAGAACAG	240
ATCTCACAGA AACGGTCTGA GTGTCCGTGG TTAGTNTCA GGATTAGTGA GAGCCAGAA	300

CCAGGTCTCA CTCGAG

316

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

```

GAATTCGGCC AAAGAGGCCT AGTCAGTCTG AGTTAGAAAA TCGACTCCAT CATCTAACAG      60
AGACTCTCAT CCAGAAACAG ACCATGCTGG AGAGTCTCAG CACAGAAAAG AACTCCCTGG      120
TCTTTCAACT GGAGCGCCTC GAACAGCAGA TGAAGTCCGC CTCTGGAAGT AGTAGTAATG      180
GGTCTTCGAT TAATATGTCT GGAATTGACA ATGGTGAAGG CACTCGTCTG CGAAATGTTC      240
CTGTTCTTTT TAATGACACA GAAACTAATC TGGCAGGAAT GTACGGAAAA GTTCGCAAAG      300
CTGCTAGTTC AATTGATCAG TTTAGTATTC GCCTGGGAAT TTTTCTCCGA AGATACCCCA      360
TAGCGCGAGT TTTTGTAATT ATATATATGG CTTTGCTTCA CCTCTGGGTC ATGATTGTTC      420
TGTTGACTTA CACACCAGAA ATGCACCACG GCCTCGAG      458

```

(2) INFORMATION FOR SEQ ID NO:457:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

```

GAATTCGGCC AAAGAGGCCT ATCGAGGTTT GGTGACTGA TCGAAGCTTT TATTTCTTTA      60
ACCATTTATG CATTCTCTCA ATTTGCTACA ATAAACATAG ATTGCACAGG GGTGAATACT      120
AAGGAACTCG GAGGGTTAGG GTTAATTTCT GTGAAAGACC AAATATGTTT CTCTGGTTCT      180
CTCGAG      186

```

(2) INFORMATION FOR SEQ ID NO:458:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

```

GAATTCGGCC AAAGAGGCCT AGCATTATGG TATATTTTAA ATTCATCAAG CTCATCTGTA      60
TGTGTCCTTT TGTCCCTTTA CTAAGTGGAG GATTGGGGCT GGGATCATGG CAGCCTGCTC      120
TGATGTATTT CTCTCCACTC TATTTTATTA TTTTCTTAAA GAGTTCTAAC TTAAATACGT      180
GGACCAGCTA TTGGATAACT TTAATTCATA TATTTATCAT TCTTTCTATT CACTTTGCCA      240
CATACACACC ATGTGATGAT TTTAAACCCG ATTTCTGTAT AGAGAATGTT AAAAGGATAG      300
CACTCGAG      308

```

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

```

GACATGCTGT GGTTCACCG CGCACTCACC CTGCTCATCA TCCTCCGCCA CTCACCAGG      60
AAGGACCCAC AGGGGCTGGG CGTGACGAGT GACGCCATCG CCGATGCCTG CCAGGCCCTG      120
GTGGGCCCCA CCGCCACAG CCGTTGCTGG TGATCTCCGG GATCCCCACC CACCTGGACG      180
AGGGCGTAGT CAGAGGCGCC ATCCGCAAGG CCTGCAACGC CCACGGCGGG GTCTTCAAAG      240
ACGAGATCTA CATCCCGCTG CAGGAAGAAG ACACCAAGAA GCCAAAAGAC AAGGCCGAGG      300
GCG                                     303

```

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

```

GAATTCGGCC TTCATGGCCT ACACTTTAAT TGCTGTTATC ATGGGCCTAA TTACAGTCAC      60
TGCAGTGGCC ACCACTGCCG GAATGGCATT ACACCACTCC ATTCAAGCGG CTCATTTTGT      120
TAATGGTTGG CAAGCCAATT CCATCCAAAT GTGGAATTCT CAACAAGGCA TCGATCGAAA      180
ATTGGCAAT CAAATTAGTG ATTTAAGACA GTCTGTTATT TGGCTTGGAG ATCAGGTAGT      240
GAGTCTCGAG                                     250

```

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

```

GGTGACGCCT GCTTCACATC TCTAATGAAC ACCCTCATGA CGTCGCTACC AGCACTAGTG      60
CAGCAACAGG GAAGGCTGCT TCTGGCTGCT AATGTGGCCA CCCTGGGGCT CCTCATGGCC      120
CGGCTCCTTA GCACCTCTCC AGCTCTTCAG GGAACACCAG CATCCCGAGG GTTCTTCGCA      180
GCTGCCATCC TCTTCCTATC ACAGTCCCAC GTGGCGCGGG CCACCCCGGG CTCAGACCAG      240
GCAGTGCTAG CCCTGTCCCC TGAGTATGAG GGCATCTGGG CCGACCTGCA GGAGCTCTGG      300
TTCCTCGAG                                     309

```

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

```
GAATTCGGCC TTCATGGCCT AATGAAGAAA AGCAGAATTC CAAATTCAAA CTGTTGGAGT    60
GAGCCAAGTG GACAGACCCT CCATGAGTGC ACTTTCTTCC AAGAAATCCC CAGATTTACC    120
CCATAGAGGT CTGGGATTAC CTGGAATATA ATATGAAAAA CATTTTTtag GCTGGGTGTG    180
GGGCTCACAC CTGTAATCCC AGCACTTTGG GAGGCTGAGG CGGGCGGATC ACCTGAGGTT    240
GGGAGCTCGA G                                     251
```

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

```
GAATTCGGAA CAATGGGGGT TTCAAACAT AAAAGTGAAA GTCCTTGTA ATCTCCTTAT    60
CCAAATGAGA AAGACAAGGA AAAAAATAAG TCAAATCTT CAGGCAAAGA AAAAGGCAGT    120
GATTCATTTA AATCTGAGAA GATGATAAA ATCTCTCCG GTGGCAAAAA GGAGTCCAGG    180
CATGATAAAG AAAAGATAGA AAAGAAAGAG AAACGGGACC TCGAG                                     225
```

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 527 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

```
CTCGAGGCGT GTGGGATCAT GAGGCAAAGA AAGTCCAACG AGGGAGAGAG GAGAGTGAGG    60
GATGAGAGGG GACACTTGCT CCATCCTAGT CCCCACGCGG CCCAGCTGGC TTCCTTTTCC    120
AGAATATCTC CTTGCTATAA CCTGGCAGCA GGGGAGCCAA GGTCTTCTC CATCCTTACA    180
GGCACTGAAC CAGGATGTAG GCGCACACTG CTGTGTTCTC TCTGGCCCAT CCTCTCTAAT    240
TGTCTTTCCC TTCCAGGTC ACAGGATGCT TATTCTCATC TCCAGGCCTT TGCACGGGCC    300
GGGCCTGCTG CCAATCCCCG CACTCTCCCC TTCTTAGGGC CAGGCTAACT CTTCCCCATC    360
CCCGGGGCTC AAGCGTTCAG GTCTCTTCCA AAAGCAGTCT TGGTGGTCCC TGCCACGCGT    420
TACCCTCCTC TCAAGTCACC CGGGAGGTGG AGGTTGCTGT AAGCCAAGAT CGCAGTGAGC    480
TGAGATTGCA CCATTGCACT CCAGCTAGG CCATGAAGGC CGAATTC                                     527
```

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GCACTCATAA AAATCTTACT CAGAAATCTT CAGAGGTTTG CTAAGGATAC AATTTGATTC	60
TTACACATTT AATGCTCACC AGCTGCTTAG GCCCACACCA TTTATCCACC CTGATTGCT	120
ACTGCTCTTT GAAATACAAC CAGTGTTC A GCCAGACTGT TTTCTGCTT CTGCTCCCCT	180
TCTCTCCTC CCAGCACATC TGTGAATTCT TTGACTGGTT TACCACTCCC AAACCTCTCC	240
CCAGCAATGC AGATCTTCTA CACCCCTTAG GATCTAAGCT AAGTCTGCTT CCCAGATATC	300
CTCCCGAACA GCTCGAG	317

(2) INFORMATION FOR SEQ ID NO:466:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 348 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GGTCATTCTT TCCATCGCTG CGGACACGGG AGTCAGAAGT GAAACAGTCC TGTCTCGTG	60
GGGCTTACGT TCCAGGCGCA AGAGCCACAG GTAGTCGAAT TGGGAACCG CCTCGGATGT	120
CACATAAGCG CCCAGGGAGG ACAGGGCAGG ACAGGGCCTC CCTGGGGAGG TGAAGTGTAGT	180
CAAGACTCAA AAGAGGGAAG CGAGGGAACA AGCCATGCGA GGAAGTAACG AAGGAACATT	240
CCAGAAAGAT TTCACATCCC AAGCCTAAG TCCAGGGGCA GCAGGCATTG AGGCGGATGT	300
GGCTGGAGTG GAGAGAAAGA GGAATTAATA GGATGGCATG AGCTCGAG	348

(2) INFORMATION FOR SEQ ID NO:467:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 293 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GAATTCGGCC TTCATGGCCT ACGAGGAAAG ATCTAATTAT CATGGACCTG CGACAGTTTC	60
TTATGTGCCT GTCCCTGTGC ACAGCCTTTG CTTGAGCAA ACCCACAGAA AAGAAGGACC	120
GTGTACATCA TGAGCCTCAG CTCAGTGACA AGGTTACAA TGATGCTCAG AGTTTTGATT	180
ATGACCATGA TGCCTTCTTG GGTGCTGAAG AAGCAAAGAC CTTTGATCAG CTGACACCAG	240
AAGAGAGCAA GGAAAGGCTT GGAAAGATTG TAAGTAAAT AGGCTGGCTC GAG	293

(2) INFORMATION FOR SEQ ID NO:468:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

GAATTCGGCC	TTCATGGCCT	AATAAATTGC	CAGCATANTA	AAAAACTGCC	TTACACTCAA	60
TTGCTACACC	TTTTCACAGG	CAAAAGGTTT	TATTCTCTCC	TAAATTAATT	TTATCCCGTT	120
TTTTTTTACC	ACCTAACTTT	TGCCTTTTAT	TCAGAACTAA	TGTATTTTTT	TCTTATTGTC	180
GTTTTTTTTT	TCAAAATTCC	CTCCTCGGTG	GAAAGTAAAG	GAGTAGGAAC	ATACTATTAT	240
TCAACCAACA	TGCAGCAACC	CTTACGTACG	GTCTCTCGAG			279

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GAATTCGGCC	TTCATGGCCT	AAGTTTTGAA	AAAAAAAATC	TTAAGTGGA	TTGTGAGTAG	60
ATTTTTTTAA	GGAGCATTTT	TATAATATTT	TTCTGAATC	CTTGCAATATT	TGACAGTGTG	120
TTTCTATTGT	GTTTATGTGT	GGCAGCAATT	TACTTTATAT	CAAAGTTTTT	TGTTTTTGTG	180
TTTGTTTTGT	GAGACACAGT	CTCACCCTAT	CACCCAGGCT	GGAGTGCACT	GGCACTATCT	240
CGGCTTACTG	CAGCCTTGAC	CTCCCACTAT	CAAGTGATCC	TCCCACCTGC	CTCGAG	296

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

GAATTCGGCC	TNCATGGCCT	ATGTTTTTTA	TATATGGATT	TATTTTTGCT	TTTTTAGGCT	60
GATTCAGTGT	GAAAATGAGG	TAGGGAAATT	GTTGTTTATC	ACAGAAATCC	CAGAATTAAT	120
ACTGGAAGAC	CCCAGTGAAG	CCAAAGAGAA	CCTCATTCTG	CAAGAAACAT	CTGTGATAGA	180
GTCGCTGGCT	GCAGATGGGA	GCCCAGGGCT	AAAATCAGTG	CTATCTACAA	GCCGAAATTT	240
AAGCAACAAC	TGTGACACAG	GAGAGAAGCC	AGTGGTTACC	TTCAAAGAAA	ACATTAAGAC	300
ACGAGAAGTG	AACAGAGACC	AAGGAAGAAG	TTTTCCTCCC	AAAGAGGTGA	GAAGGGACTA	360
TAGCAAAGGA	CTCGAG					376

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

GAATTCGGCC	TTCATGGCCT	ACAAGATTGG	CAAGATGCTT	ATTTTGGTG	CCATATTGG	60
CTGCCTTGAC	CCAGTGGCAA	CACTAGCTGC	AGTTATGACA	GAGAAGTCTC	CTTTTACCAC	120
ACCAATTGGT	CGAAAAGATG	AAGCAGATCT	TGCAAAATCA	GCTTTGGCCA	TGGCGGATTC	180
AGACCACCTG	ACGATCTACA	ATGCATATCT	AGGATGGAAG	AAAGCACCAC	AAGAAGGAGG	240
TTATCGTTCT	GAAATCACAT	ACTGCCGGAG	GCTACTCGAG			280

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GAATTCGGCC	TTCATGGCCT	AGCAGTAAGC	CAGGATTGCA	CCACTGCACT	CCAGCCTGAG	60
TGACAGAGTG	AGACTCTGTT	TCAAAACAAA	ACAAAAAACT	TTACAGCAAT	CCTGGTCCCT	120
ACCATGGAGC	ATGTGTTACA	GGAAAACAGC	CAGTCCACTC	TGCAACCAAT	TTGGACATGG	180
CCCTGAAAAT	CCTTTTGTGA	CAGAAAGGGG	AAAATAAGAG	TACTGGCAGA	AAGTCAGATG	240
CTGGGGATGC	CTCACCTCT	AGTCTCATGA	CTATCACACA	TGAGACGGTG	TTCCGCTGTA	300
ACTTTTCCCC	CCCCCCCCC	CGTTGTGGA	TCTGAATCTG	GAAAAGAGCT	TGGAGAGATT	360
TACAGGCCTC	CTCTTCTGCA	ATCAGTAAGA	GTACCATGTG	GAGGCAGAGA	GCCAGAATAG	420
GTTGTGGGGC	TTCTCGAG					438

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GAATTCGGCC	TTCATGGCCT	AGAACAGCTC	TCCAATTCAC	ACTTATCTGT	ACAATGTACA	60
TTAATAACTA	ATTGTTAGA	TGATTAATAC	CAATAATTAA	CTTGCTAGAG	GACCCAGGAA	120
ACAGAATATC	TGCAAGGCCC	AGAGTAGATC	ATAAATAAAT	AGGAATGCAG	ACATAAGATG	180
TTCAGTTTGT	GAACAGTAAA	GCTATAATGA	GTTTTCTTTA	AAATCAAACA	ATTGTACAAT	240
GCATTATAGT	CTACAACCTA	TTCTGTAGTT	CAAATAAATA	AACTTTCCC	CTGTTACAGA	300
AAGACAGCCC	TCCTCCCAGC	AACATTTCAG	ACTGGATGGA	TTGATTCCTC	ACCTGACATA	360
ACTCTAAAT	CCTCACTGAA	GAAGCCAGGA	AGTCAAACCTG	AGGCTGAAGA	CCTGAAAGTA	420
CAGGGGACTA	AACCCAGAAA	GCAGTAGGCC	ATGAG			455

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GAATTCGGCC	TTCATGGCCT	ACATGGACCT	CCTGCACAAG	AACATGAAAC	ACCTGTGGTT	60
CTTCCTCCTC	CTGGTGGCAG	CTCCCAGATG	GGTCCTGTCC	CAGGTGCAGC	TACATCAGTG	120
GGGCACAGGA	CTGTTGAAGC	CTTCGGAGAC	CCTGTCCCTC	ACCTGCGCTG	TGAATGGTGA	180
GCCCTTCAGT	GGTTATTTCT	GGACCTGGAT	CCGCCAGNCC	CCCGGGAAGG	GCCTGGAGTG	240
GATTGGGCAA	ATCAATTATG	ATGGAACCAC	CAAGCACAAC	CCCTCCCTCG	AG	292

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GAATTCGGCC	TTCATGGCCT	AAGGGTGGGC	TTTAATGGCA	GCTGGGGTAA	AAGGAAACAA	60
AAACAGTAAT	TCTGAAGAGC	ACAGGGAACA	GGCAGCCAGG	ACCAGCCTGG	CCCATTCCAG	120
GCCAGCTGAG	CTGAAATGCT	GATTCTGTCC	AGGGGGCTGC	TGTATGTGTA	GACTGGTGGC	180
AGTCTTGGGG	ACTGAGGCCT	CTTGAGAGAG	AGGGAAGACT	GTCGGCTCAG	AAGTCCATGG	240
AGCTGTGGGC	CAGGTAGTCC	TTGCCACCGA	TGTTGCTGAC	CTGCTTGGTC	TGCATAGCCT	300
CGAG						304

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GAATTCGGCC	TTCATGGCCT	ACCAGCTCTC	TTCTAAAAGA	GAAGTGGGTG	GGCACACTGA	60
ACTGTTTGGT	GGCCCCAACC	ACAGGAAGCT	GCAATTCTCT	GGCTTAGGGT	GATACTTTTG	120
CCCTCCTTGT	GCCCCCTCTC	GGACGCTCTG	CACCAACCCC	AGGCTACTGA	GCCACCTTCC	180
CTCCTCATGC	CTTCCCTGAG	CTTTGGTGCA	TCTCATCTGG	ACTATGGGTT	GTACTGTGAC	240
CATCCCAACA	CCTCACCTC	TGTCTACAAG	GAAATGGGAG	GTGGAGCCTC	CTGGCTGAGA	300
AATTGTTTTG	CAAATGGATC	TCGAG				325

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GAATTCGGCC	TTCATGGCCT	AAGCTCATCA	ACGAGAAGCT	CATCAGAACC	AAGGGGCTGT	60
GGGGCCCCGT	CCATGAGCTG	GGCCGCAACC	AGCAGCGGCA	GGAGTGGGAG	TTCCCAACCAC	120

ACACCACCGA GGCCACCTGC AACCTGTGGT GTGTGTATGT GCATGAGACG GTCTTGGGCA	180
TTCCTCGAAG CCGTGCCAAT ATTGCTCTGT GGCCCCAGT TCGGGAGAAG AGAGTCAGAA	240
TCTACCTGAG CAAGGGTCCC AATGTGAAAA ACTGGAATGC ATGGACCGCA CTGGAAACTC	300
GAG	303

(2) INFORMATION FOR SEQ ID NO:478:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GAATTCGGCC TTCATGGCCT AGTTGTTTCTAG AATCCACACA GCTCTGAATT ACCAACGCTG	60
AATTTCCAAG ATACTGTAAA CACCTTGACC AACAGTCCAG CCATCCCATT GGAAACATCT	120
GCATGTCAGG ACATACCCAC TTCTGCCAAT GTACAAAATG CAGAGGGTAC CAAATGGGGA	180
GAGGAGGCAT TGAAAATGGA TCTTGACAAT AACTTTTATT CAACTGAGGT GTCAGTTTCT	240
TCCACTGAAA ATGCTGTCAG TTCTGACCTC CGGGCAGGGG ATGTACCTGT TTTATCTTTG	300
AGTAATAGCA GTGAGAATGC CGCCTCTGTG ATCAGCTCGA G	341

(2) INFORMATION FOR SEQ ID NO:479:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 296 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GAATTCGGCC TTCATGGCCT AAGTTTTGAA AAAAAAATC TTTAAGTGA TTGTGAGTAG	60
ATTTTTTTAA GGAGCATTTT TATAATATTT TTCTGAATC CTTGCATATT TGACAGTGTC	120
TTTCTATTGT GTTTATGTGT GGCAGCAATT TACTTTATAT CAAAGTTTTT TGTTTTTGT	180
TTTGTTTTGT GAGACACAGT CTCACCCTAT CACCCAGGCT GGAGTGCAT GGCACATCT	240
CGGCTTACTG CAGCCTTGAC CTCCCAGACT CAAGTGATCC TCCCACCTGC CTCGAG	296

(2) INFORMATION FOR SEQ ID NO:480:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC	60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATA ATCAGTTCCC TTTGCCGAGA	120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA	180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA	240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA	300

CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA 360
CTTACCCATG GGAACCTGAG 380

(2) INFORMATION FOR SEQ ID NO:481:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GAATTCGGCC TTCATGGCCT AAGTTTGTAA AAAAAAATC TTAAAGTGA TTGTGAGTAG 60
 ATTTTTTTAA GGAGCATTTT TATAATATTT TTCCTGAATC CTTCATATT TGACAGTGTC 120
 TTTCTATTGT GTTTATGTGT GGCAGCAATT TACTTTATAT CAAAGTTTTT TGTTTTGT 180
 TTGTTTTGT GAGACACAGT CTCACCTAT CACCCAGGCT GGAGTGCAT GGCATATCT 240
 CGGCTTACTG CAGCCTTGAC CTCCAGACT CAAGTGATCC TCCACCTGC CTCGAG 296

(2) INFORMATION FOR SEQ ID NO:482:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC 60
 ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATA ATCAGTTCCC TTGCGGAGA 120
 ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA 180
 AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA 240
 GGAAGCCCTA TGCTGAGAGG GTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA 300
 CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA 360
 CTTACCCATG GGAACCTGAG 380

(2) INFORMATION FOR SEQ ID NO:483:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GAATTCGGCC TTCATGGCCT AGGCTGGACA GACTTTCTAA TGAACCCAAT GGTTATGATG 60
 ATGGTTCTTC CTTTATTGAT ATTTGTGCTT CTGCCTAAAG TGGTCAACAC AAGTGATCCT 120
 GACATGAGAC GGGAAATGGA GCAGTCAATG AATATGCTGA ATTCCAACCA TGAGTTGCCT 180
 GATGTTTCTG AGTTCATGAC AAGACTCTTC TCTTCAAAAT CATCTGGCAA ATCTAGCAAC 240
 GGACAGCTCG AG 252

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

```

GAATTCGGCC TTCATGGCCT ACTACATCAA GCACCAGAAC CGCCAGCTGC GCGCCCTGTT      60
GCTCAGCCAC CAGTTCAAGC GCCGGGAGGC CGACCAGACC CACGCACAGA ACTTCTCTC      120
CGCCGTGAAG TCCCCGGTCC AGGTCACTCT GTCCTGTGCC CTCGCCTTCC TGGCCTGCGC      180
CTTCTACTG ACCACCGCGC TGTATGGGGC CAGCGGACAC TTCGCCCCAG GCACCACTGT      240
GCCCCTGGCC CTGCCACCTG GTGGCAATGG CTCAGCCACA CCGACAATG GCACCAGGCT      300
CGAG                                                                    304

```

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTGCGCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTCGAG                                                                    380

```

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTTGGCATAAC ATCAGTTCCC TTGCGCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAACCTCGAG                                                                    380

```

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTGGGCATAC ATCAGTTCCC TTGCGCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAAGTCGAG

```

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

```

GAATTCGGCC TTCATGGCCT ACAGAGATGG ATTATCCTAC TTTACTTTTG GCTCTTCTTC      60
ATGTATACAG AGCTCTATGT GAAGAGGTGC TTGGGCATAC ATCAGTTCCC TTGCGCGAGA      120
ACATGTCTCT AGAATGTGTG TATCCATCAA TGGGCATCTT AACACAGGTG GAGTGGTTCA      180
AGATCGGGAC CCAGCAGGAT TCCATAGCCA TTTTCAGCCC TACTCATGGC ATGGTCATAA      240
GGAAGCCCTA TGCTGAGAGG GTTTACTTTT TGAATTCAAC GATGGCTTCC AATAACATGA      300
CTCTTTTCTT TCGGAATGCC TCTGAAGATG ATGTTGGCTA CTATTCCTGC TCTCTTTACA      360
CTTACCCATG GGAAGTCGAG

```

(2) INFORMATION FOR SEQ ID NO:489:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

```

GAATTCGGCC TTCATGGCCT AGGTTTACAG GCATACCTCA TTTTATTGCA CTTCACTTTA      60
TTGTGCTTTG CAGATAATTG TGCTTTTAC AAATTGAAGG TTAGTGGCAA CCCTGTGTTG      120
AGCAAGTTCA TTGGCAACAT TTTTCCAACA GCATGTACTC ACTTGTCTCT ATGTCACATC      180
TTGATAATTT TCATATTTCC AACTTTTTC TTATCATGAT GATGATTAGT GATCTTTGTT      240
ACTGTNGTAG TTGTTTGTG GGCACCACAC TGTATGCAGN AAAGCTCGAG      290

```

(2) INFORMATION FOR SEQ ID NO:490:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

```

GCTACCTTAA AAAATAGATA CTCCACTAGA GGCTGTGCTT AATTCAAATC CATGTGTGTG      60
CCTGCATTAC ATGTGTGAAC ACGTGTTTCT GTCGTGTGTG TCATGCACAT CTGTGTGTTG      120
CATAGCATAA GCCAAATGAA AATCATTTGT TCATGGGATT CATATGAGGA ACAAATTTAA      180
ATTTGAATAC AGTCAGATAA CTGCCACGCA GGGCATTGTT GGAACCATCC CCGAATGCCG      240
TGATGTGATT TCCCTCAGAA AATCCTTGTT ATTAGAGGAG AAGGTCTGGG CAGGGGCAGC      300
AGCATCTCAG ACATCAAGTC AACTTTATCA TCTACTACAT CAGCACTGAA GTCCAACGGC      360
ATCCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:

```

GAATTCGGCC TTCATGGCCT ATGCTTTTTT CTTTATCTTT TGTAGTTGTT TAGGAGTGGG      60
GGGCC'CTGCA GAACACCTAG TCCAGCCCAC TGCCAGAGC AGGTGTGTCC CTTTCATACT      120
TCAGTCCACT TTAACACAGC CTTCCCCCAC CCCCTTCTAT GGTAGCAGTT CTCCTCGGGG      180
TCTCCATGGA CACCCTGTGC CCCAAGCCGA TGGCCCCACC CAGCAGCATC AGCACAGCTG      240
CCCCCTTCT CCGCAGAGCA GGCTCTCCTT TACGGGACTC TCCTCTTCCC TCCCACCCCC      300
CCTCGAG

```

(2) INFORMATION FOR SEQ ID NO:492:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:

```

GGAATAAGAA GAGAAAGCCA AGGAAGACAA GGGCAAACAA AAGTTGAGGC NGCTTCACAC      60
ACACAGATAC GGAGAANCCA GAAGTGCCAG AGTCAGCATT CTGGAAGAAA ATCATAGCAT      120
ATCAACAGAA ACTTCTAAAC TATTTTGCTC GCAACTTTTA CAACATGAGA ATGTTAGCCT      180
TATTTGTGCG ATTTGCTATC AATTTTCATCT TGCTCTTTTA TAAGGTCTCC ACTTCTTCTG      240
TGGTTGAAGG AAAGGAGCTC CCCACGAGGC TCGAG

```

(2) INFORMATION FOR SEQ ID NO:493:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:

GCCTTGGGCC	CTCGCAAAGT	CTTGGAGAAG	CAGTTTACT	TCCCTTCCTT	CACTTAGACC	60
CCATTCTTTA	GCATTTCTTC	TGAAGCTCCC	ACAAGACCCA	AGAATGGCTG	CTGCAGTGTC	120
TCCTCTTCAG	TCAGGGACCC	TGGTTGAGGT	TTGTGTATTG	TTCATTATTG	CTCTGTTTTG	180
CAGTTGTCA	AAGTTGGAAG	ACTTGCCTGC	GGAGCAGTGG	AACCATGCCA	CAGTCCGCAA	240
TGCCTTAAAG	GNACTGCTCA	AAGAGATGAA	CCAGAGCACA	TTAGCCAAAG	AAACCTCGA	300
G						301

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

GGAAGATGTC	TACAGAAAAG	GTAGACCAA	AGGAGGAAGC	TGGGGAAAAA	AGAGTGTGCG	60
GAGACCAGAT	CAAGGGACCG	GACAAAGAGG	AGGAACCACC	AGCTGCTGCA	TCCCATGGCC	120
AGGGGTGGCG	TCCAGGTGGC	AGAGCAGCTA	GGAACGCAAG	GCCTGAACCT	GGGGCCAGAC	180
ACCCTGCTCT	CCCGGCCATG	GTCAACGACC	CTCCAGTACC	TGCCTTACTG	TGGGCCCAGG	240
AGGTGGGCCA	AGTCTTGGCA	GGCCGTGCCC	GCAGGCTGCT	GCTGCAGTTT	GGGGTGCTCT	300
TCTGCACCAT	CCTCCTTTTG	CTCTGGGTGT	CTGTCTTCCT	CTATGGCTCC	TTCTACTATT	360
CCTATATGCC	GACAGTCAGC	GCACTCGAG				389

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 438 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

GTGGCGATTG	GTCCTGTCAT	GGTTATTCA	GCCATGTGGT	GGATGGCTAC	TTGTCTTCTA	60
AGCCACTTGC	CTTCTGATCG	CTGGACTGAC	TCTCTCGCCC	TCTCTTGGTG	CAGTCCTCAG	120
GAGGCTCGGT	CACACTCTCC	AAGAGCACAG	CCATCATCTC	CCACGGTACC	ACAGGCCTGG	180
TCACATGGGA	TGCCGCCCTC	TACCTTGCA	AATGGGCCAT	CGAGAACCCG	GCAGCCTTCA	240
TTAACAGGTG	ACCTCGGGGC	ACAGGGCAGG	GCACCGAGGC	AGGCTTACCC	TGGTGCAATC	300
GAAACACGG	TCCCCCTTCC	TCCCGCCAGG	ACTGTCTTAG	AGCTTGGCAG	TGGTGCCGGC	360
CTCACAGGCC	TTGCCATCTG	CAAGANGTGC	CGCCCCCGGG	CATACATCTT	CAGCGACCCT	420
CACAGCCNGG	TCCTCGAG					438

(2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

```
GAATTCGGCC TTCATGGCCT AGGTAAAATT TGTATAACAA AAAATTAACC GTTTTAACT      60
GAATAATTCA GTGAGATTTA GTGAATTCAC AATATTGTGC AACTGCCACC TCTTTCTACT    120
TCTAAACCAT TTTCTCATA CCAAAAGTAA GCCCCGTACC TATGATGCAG TCCCTTCCCG     180
TTTCTTCTC TCCTCAGTCC CTGGCAACCA TCACTCTGCT TTCTGTCTCT GTGGATTAC      240
TTATTCTAAT ATTTAATTC AGTGGGAATC CCTGCCTCGA G                          281
```

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

```
GAATTCGGCC TTCATGGCCT ACACTTAGAG AGGCAGTCGG GATGGAGGGT CGAGTTGAAG      60
ACAGGGAGGG GTGAGGAACG AGCAGAGGCC AGTTGTTTGG CCACTTGAGG GAGTTTGGAC     120
TTGTCCCAGG GGCAC TAGGG AGCCGTGAAG GGCTTCAAGC CGGGGAGGAT CATGAACATT     180
TCCCCAGAGG AGCTCAAAAT GGAGTTGCCG GAGAGACAGC CCAGGTTTCGT GGTTCACAGC     240
TACAAGTACG TGCATGACGA TGGCCGAGTG TCCTACCCCTT TGTGTTTCAT CTTCTCCAGC     300
CCTGTGGGCT GCAAGCCGGA ACAACAGATG ATGTATGCAG GGAGTAAAAA CAGGCTGGTG     360
CAGACAGCAG AGCTCACAAA GGTGTTTCGAA ATCCGCACCA CTGATGACCT CACTGAGGCC     420
TGGCTCCAAG AAAAGTTGTC TTTCTTTCGT TGATCTCTGG GCTGGGGACT GAATTCCTGA     480
TGTCTGAGTC CTCAAGGTGA CTGGGGACTT GGAACCCCTA GGACCTGAAC AACCAAGACT     540
TTAAATAAAT TTAAATGC AAAACTCGAG                          570
```

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

```
GAATTCGGCC TTCATGGCCT AGGTGCATGC CATCAAATAC TCTAACGAGA CATTTTAAAT      60
GAAAGACTTA AACCAGATAG GCCACAATGA ACCAAATTAG AAATCTGAAC ATGTCACCAC     120
TTGCAGCATA AAGGAATATA AAAGGGCAGA GCAAAGTCTT TTTTCCTAAG GTGAATATTT     180
CTAAGGTAAG TATTCATTG TAAAAGTTT TTTTTCAN CANGTCTGAA NNCTTTTAC      240
CANNNGGNGA GNATTACAAC AAAACATCCC TNGGTTAAAA AAAAAAATA CCATCTTGCA     300
ATTCAGCACA CACCNGCAGC TGGTGTGCTC ATCCAACCN ATCAGTAGGC TAAGAGNATT     360
TNAATTCCA TACATATGAG TTTAGGTATT AATGCCGATT ACACAGTACA CAGTACAGAG     420
GGAGGTCCCT ATATCCACAC ACACACACAC CCCATCCAGC ATTTACACCN AAAGCCTTAC     480
CCTCGAG                          487
```

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

```

GAATTCGGCC TTCATGGCCT AACAAATCAA AGAAACTTTT TTCTGAACCA TTTGAAATTT      60
GCCAGCCTGA TGTCCCATCA CCCCCCAAGT ATTTTAGCAT CTATGCAACA AAACATTTTC      120
TCTGACAAAA CCACATCAGA ACTCTCAAAT CAGGAAACAA ACATTGATAC ATGTCTATCA      180
ACTAATCCTG TCTTCAATGA CATTTTACCG ATTGTTCCAA TGATGTCAGC ATCACGGGTC      240
ACATTTAATA GTTGGCTCCT TCAGTCTCGA G                                     271

```

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

```

GCACTTCTGG ATGTTGGTTC TCTTTGTCAT TTTCAACAGT CTGCAGGGAC TTTATGTTTT      60
CATGTTTTAT TTCATTTTAC ACAACCAAT GTGTGCCCCT ATGAAGGCCA GTTACACTGT      120
GGAAATGAAT GGGCATCCTG GACCCAGCAC AGCCTTTTTC ACGCCCGGGA GTGGAATGCC      180
TCCTGCTGGA GGGGAAATCA GCAAGTCCAC CCAGAATCTC ATCGGTGCTA TGGAGGAGGT      240
GCCACCTGAC TGGGAGAGAG CATCCTTCCA ACAGGGCAGT CAGGCCAGCC CTGATTAA      300
GCCACGTCCA CTCGAG                                     316

```

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

```

GACAAAGACC AGCAATGGAT CACTTGGAGT CCTTTATTGC TGAATGTGAT CGGAGAACTG      60
AGCTCGCCAA GAAGCGGCTG GCAGAAACAC AGGAGGAAAT CAGTGCGGAA GTTTCCTGCAA      120
AGGCAGGAAA AGTACATGAG TTAATGAAG AAATAGGNAA ACTCCTTGCT AAAGCCGAAC      180
AGCTAGGGGC TGAAGGTAAT GTGGATGAAT CCCAGNAGAT TCTTATGGAA GTGGNAAAAG      240
TTCGTGCGGA GGAAAAGGA GNACTCGAG                                     269

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```
GAATTCGGCC TTCATGGCCT ACTTGTCTCA CTCTGCATCA TCCCTTAGTC TACAACAGGC      60
CTTTTCTGAA CTTAGACGTG CCCAAATGAC AGAAGGACCC AACACAGCAC CTCCAAACTT      120
TAGTCATACA GGACCAACAT TTCCAGTAGT ACCTCCTTTC TTAAGTAGCA TTGCTGGAGT      180
CCCAACCACA GCAGCAGCCA CAGCACCAGT CCCTGCAACA AGCAGCCCTC CTAATGACAT      240
TTCCACATCA GTAATTCAGT CTGAGGTAC AGTGCCCACT GAAGAGGGGA TTGCTGGAGT      300
TGCCACCAGC ACAGGTGTGG TAACTTCAGG TGGTCTCCC ATACCACCTG TGTCTGAATC      360
ACCAGTACTT TCCAGCGTAG TTTCAAGTAT CACAATACTC GAG                          403
```

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

```
GTTTGGATGA TTGGTGGCGT GTACGCAGCT GCTATGGCCT GGGCCATCAT CCCCCACTAT      60
GGGTGGAGTT TTCAGATGGG TTCTGCCTAC CAGTCCACA GCTGGAGGGT CTTCTGCCTC      120
GTCTGCGCCT TTCCTTCTGT GTTTGCCATT GGGGCTCTGA CCACGCAGCC TGAGAGCCCC      180
CGTTTCTTCC TAGAGAATGG AAAGCATGAT GAGGCTGGA TGGTGCTGAA GCAGGTCCAT      240
GATACCAACA TGCGAGCCAA AGGACATCCT GAGCGACTCG AG                          282
```

(2) INFORMATION FOR SEQ ID NO:504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:

```
GAATTCGGCC TTCATGGCCT ACTGAGAAAA AAAATCAAAT CTAATTTTAA AATGAAGGTA      60
TTTAAACCA TGGCACAAGG GAGCCTTATT TATGGAGCTG GTGGGAAGCC AGGATGTTTC      120
CAATCCGCTG CTCTTACAGG AGCCTGTGCC TCGCCAGTTC TGTGCTGCAG TGGGCAGCCA      180
ACTGAAGTGC ATGAGTCAA TGCACGAAGC AGCAGACTCG AG                          222
```

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

GAATTCGGCC TTCATGCCCT AGTGGTGAG TTTTTCAGGA TTGTAGAGAT GCTAACAAAT	60
TACAGGTTCT CTCATGCAAA CACTTTGCTA GGAATTATAT ATATCAAGTT TATATTTGGC	120
AATCAGGCTT TAGAAGCAGA AGGTCTAGCT ATCTCAAACCT ACCACCTACC TCCCTCACCA	180
AAGCCGCTCG AG	192

(2) INFORMATION FOR SEQ ID NO:506:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

GAATTCGGCC TTCNTGGCNT AGTAAAATTG TTAAAGTTCA CAGGATCAGT TTTGGAAGAT	60
GCTTGAAGG AAAAAGCAAA GATGGATATG GAAGAAATTA TTCAGAGAAT TGAANACGTT	120
GTCCTAGATG CAAACTGCAG TAGAGATGTA AGACAGATGC TCTGAAGCT TGTAGAACTC	180
CGGTCAAGTA ACTGGGNCAG AGTCCANGCA ACTTCAACAT ATAGAGGNGC NACACCAGAA	240
AATGATCCTA ACTACTTTAT GNATGNACCC ACATTTCATA CATCTGATGG TGTTCCTTTC	300
ACTGCAGCTG ATCCAGATTA CCANGAGAAA NTCCAAGAA NACTTGAAAG AGANGATCCT	360
CGAG	364

(2) INFORMATION FOR SEQ ID NO:507:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

GAATTCGGCC TTCGATTGAA TTCTAGGACT TGACAGAATT CGAGTTATCC TTCTCAGAAC	60
ATGTGCAGAG TCTCTTTTGG CCTCACCATG TGGTCCTGTG CTCCTTCAGG TGGGAGTTT	120
GGGGCCTCCA GGGCAGCAGG CACCACCTCC ATATCCCGGC CCACATCCAG CTGGACCCCC	180
TGTCATACAG CAGCCAACAA CACCCATGTT TGTAAGCTCCC CCCCAAAGAC CCAGCGGCTT	240
CTTCACTCAG AGGCCTACCT GAAATACATT GAAGGACTCA GTGCGGAGTC CAACAGCATT	300
AGCAAGTGGG ATCAGAGCAA TCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:508:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:

GAATTCAGTG AGTGGGCATG GCTGATCTTG TGCAAATTAA AAGTTATGGG GCATAAGAAT	60
AGCAAAAGTT GAACTTCTTT TAAAAAGGAA AGTACCCTGA GAGCCAGTAT TGGTTGAGGC	120
TCTTCAGTAT GCCCAGGTTG GCAGCACTGA GAACCGCAGG AACGGCCTGT TGTTACAAAA	180
AGGAGATTGA CTCAGCTGCC CTTGGTGCAT CTGACTGACT ATGACTGCTG AGAGATTCCA	240
AGGACCCTTA ATGCCAGGGC TAACCTCTCC ATGTGCAGTG AGACCTCTGG AGGAAGTGTC	300
ATCCTCTGGC TTTGTGTGGT ACTCATTATG GTGCAGTGCC GGCATGAAAT GAAGACACAC	360
AAATAGGCTC GAG	373

(2) INFORMATION FOR SEQ ID NO:509:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:

GAATTCGGCC TTCATGGCCT ACTCTTCCTG GCTCCTTCTC AGCCTTGTTG CTGTAAGTGC	60
TGCTCAGTCC ACCATTGAGG AACAGGCCAA GACATTTTGG GACAAGTTTA ACCACGAAGC	120
CGAAGACCTG TTCTATCAAA GTTCACTTGC TTCTTGGAAT TATAACACCA ATATTACTGA	180
AGAGAATGTC CAAACATGA ATAATGCTGG GGACAAATGG TCTGCCTTTT TAAAGGAACA	240
GTCCACACTT GCCCAAATGT ATCCACTACA AGAAATTCAG AATCTCACAG TCAAGCTTCA	300
GTGCAGGCTC GAG	313

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

GAATTCGGCC TTCATGGCCT ACTTGAACAA TTAAATATA GGAGAAGACT ATTTTITAGA	60
AATGTTTTCG GTCCGCAACT TGTAAAGCT TTATAGCACT TTGCATATTT TGGAGAATGT	120
CAACTATATT TTTATCAGAG CTGATTGTGTT CCAGTGGAAC AACAGTGCGG TAGACATCGC	180
CCACAAGGTT CTGCATACTC GAG	203

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

GAATTCGGCC TTCATGGCCT ACGTGGTATT AAGGAGACAA TCTGAGGCAT TCCCACCACT	60
CAATTTGACA TGCGGTTGGC AAGGTTTCCTC TTCCTTCCC ACTTTAGATC GTGCCCTGTC	120

CCAGGTCAGA CCCGAAAGAT TCATAGGCAC ACTTACAGCC TTCATAGTCT CAGCCATAGT	180
CATCCTAGCA ACTGCTAGTG TGGCTGTAGC ATCTATTACT GAATCAGTAC AAACAGCTGC	240
TTTTGTAGAT AATTTGGCCA GAAATGTTTC TAATGAACTT CTCTTACAGC AAGGTATAGA	300
TCAAAAGATT CTTGCACATC TGCAAGCCCT CGAG	334

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

GAATTCGGNC TTCATGGCCN AAAGCTCTNG AAGGAGTATT AGAGTACAGA GTCTGAGNCT	60
NTGANAAATG GTGGTCAGAA GCCNTCTTCA TCAGATANAT TTCTCAGATG TGCCCCCTTC	120
GCGGCAGAGG NGGATATTCA TCTCCTAGTT CATGTTTCTG AACATGTCAG TANGCAGATN	180
ANTCACTACC AGTATCTGCT TCTACTTTTC CTGCATGAGT CACTTATCCC TGCTTTCAGA	240
GAACNTAAGG AAAGATGTAG AAGCTGTAAC TGGCAGTCCT GCTAGTCAGA CATCCATTG	300
TATTGGAATT TTACTTAGAA GTGCAGAACT GGCTCTTTTG CTCCATCCAG TGGATCAAGC	360
AAATACTCTT AAGTCTCCTC TTTCTGAAAG TGTGAGCCCA GTGGTACCTG ANTATTGCG	420
TACAGAAAAT GGGGATTTTT TGNCCCTCAA AAGAAAACAA ATTAGTAGGG ATATAAATAG	480
AATTAGAAGT GTAAGTGTTA ATCATATGTC AGACAACAGA TCTATGAGTA TCTCGAG	537

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

GAATTCGGCC TTCATGGCCA AGGTGCTTAA TATTAAAAA AAAAAAAGTA TATCCAACCA	60
CAGATATACA GTTCTGCCTT TTTTCCTTT TTACCTAAAT ATACTCCATA AACAGTTTCC	120
ATGTTGTGTA ATATCTTCAT GTTCTACTT TTCAGTGATT GCTTAAATGT CCATTGGGCT	180
GATAGGTCAC AGTTCGCTAA CCCATCTCAT TGTTGTTCAT TGGGATCTCC ACTTCCCTC	240
GAG	243

(2) INFORMATION FOR SEQ ID NO:514:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

GAATTCGGCC TTCATGGCCT AGTCTCAAAA AAAAAAAAAA GATTATCCAC AAATGCAGTG	60
GNCCCTGGGA CAAGCCCTTT AAAGGAGTCA TNGAGAATCG TCTGTTGCTC ACAGCATCAA	120

TCNGGTATTT AGTTCTCAAG CTGAGGATT CTAGTTTTCG TCAGAGGGTC GGGTTCAGTC	180
TCTAAAAGAC GCTCTGAAAG CAGACCAGGC TGTTTCTTG GAGCTTTTCA GGTTAGATTC	240
TCATGTGTGT ATCTTCCATC TACCACGATT ATTGGCTAC CAGATGCCTT AGCAAGCTGA	300
ACAGTGAGCT CAGAAGTGCC ACCATCTATA GTAACATTCT CGAG	344

(2) INFORMATION FOR SEQ ID NO:515:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:

GAATTCGGCC TTCATGGCCT AAGAGTATCC GCTTACAGAA AAGACACTTC ATCACCTAGC	60
ACTGATTAT GCAGCTTTGG TTTCATTTGG GCTAACTCT GAAGAACTGG ATGTAAAGCT	120
TATAATTGCC CCAGGAGTAG AAGCAACTGC CTTGATAATT CGACAAATTG CTGACCACAG	180
TTTAATGACC TCAAAGAGAG ATCCTCATGA ATGTTGGAT AAATCCTGGC TTAAAGTTTC	240
ACCATCTGAG GAAGAAATGT ACTTACTTGA TTTCCATGT ATTAACCCAA TCGTGGCTCG	300
AG	302

(2) INFORMATION FOR SEQ ID NO:516:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:

GAATTCGGCC TTCATGGCCT ATAGGCCATG AAGGCCGGCC TTCATGGCCT AATCCATAAA	60
AGGCTTTTGA GATGTCTCTG CTGAAAATAA ATGCAGCTCT AGTAAATGTT AGAGTTTTCG	120
CTAGTAGAGT TTTGATGCTT TTTGTCTTG TTTACTACT GAGCTTGAC CTAGGATGCC	180
TTCTTATAGT GCCATTCAAC ATGCAAGTTT CTTTTCCTGG GGCTGTGTGT CCAGGTGACT	240
TTATGAGTTA GGCTTTGGCA AATGCCAGAC TTGTTCATCC TAACACTAGA ATGTAGGGAT	300
CCTGCATTCA GCATGACCCT CGAG	324

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

GAATTCGGCC TTCATGGCCT ATAGGCCANG AAGGCCGGCC TTCATGGCCT ATAGGCCATG	60
AAGGGTTGGT TGTGTTTTCC TAACAATGAA TAAGACAGAA ACCCTTGATA GCTAAATTCA	120
TCTGCAGTCA AACTAAGTTT TGCAGTGTCT TTTTAAGAGC CAGGCAATTC TACCACAAAA	180
TAAAATATAT TTTTAAATC CACATTACTA TACCACTGAC AAGTCTTTAC TTCAGAACTC	240

ATCATTCAGA AATGTGTAGC TGCTTCCAGA GTGTGTCTAA TACTGTTGGA ACAGGCGTTT	300
CAGAAAGAAA TGAGAGGCC AGTCTCAGTA ACTCCATGAA GGGTGCCGAG CTCCTCTGTT	360
GAGGATTTGG CTTGTGAGAG GCAATGTTCC TATCATTTGC CAATTTGGCC TTTGTTATTC	420
CCACATTGGC TCGAG	435

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

GAATTCGGCC TTCATGGCCT ACCAGGTTGG CCAGGCTGGT CTCGAACTCC TGACCTCAGG	60
TGATCTGCTC ACCTCGGCCT CTCAAAGTGT TGGGATTACA GGAGTGAGCC ACCGCACCGG	120
GCCAAAAAAT CCAATTTCTT AGAGATTAAA TAACCTTCA GGATTATCAA AGGAAATAAT	180
TAGGGAAGG TAGATGTTCT GTCCAGTAA GAGAAGAAAG TGGTCCAGAA ATTTTATCTC	240
CCATCAAATG ATCCATTTTA CTTAAAGTATT AAACCAAGTG ACATTCTTCA GTTTAACTCT	300
GATAAATGAA TCATATTCCT CTTGAAAAT AACTTTTGTA TTTCGTGCTC TAAAAAGAGA	360
ACCACCCCTC GAG	373

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 397 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

GAATTCGGCC TTCATGGCCT AAACAATTAA TTGTGGGTGT CTGAGGGGGA AGGTCGCAGC	60
TTTGGGCAGC TTTGAGAAGC GGTACAAGAG TTCTGTGCCT GTGTGTCCAG CCCTGGAGCC	120
AGCCAGTGCA TTTATTTTAA GCTCTTAGAA GCAACTCCTT GGCCAGGAA TGCCTGACCC	180
CTGAGATGGG TCCACGCATC TCTTACACT TCCTTCTCTC CGTGGGATAC TGGACTCGTG	240
CCTCTGCGCC CATTCTCTTC TCACGCATAT CCATGAGCTT TAATTTCACT TTCTGATCAC	300
GGTACGTCCA TAAAGCCAGT ATTACACTTA AATGAAGTAT TCTTTTTTGT AATCGTTTTT	360
TTTAGAAGGT AAACAAATTT AATAAAGCTA TCTCGAG	397

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

GAATTCGGCC TTCATGGCCC ACATGAATCT NGTAATTTGT GTCCTACTTT TGTCCATTTG	60
GAAAAATAAT TGCATGACTA CAAACCAAAC CAATGGATCT TCTACTACAG GAGATAAAC	120

TGTGGAATCA ATGCAGACAA AATTGAACTA CCTTAGAAGA AATCTACTCA TTTTAGTTGG	180
TATTATCATC ATGGTTTTTG TCTTTATCTG TTTTGTAT CTCCATTATA ATTGTCTGAG	240
CGATGATGCG TCCAAAGCAG GAATGGTCAA GAAAAAAGGC ATAGCAGCCA AGTCATCTAA	300
AACATCATTC AGTGAAGCCA AGACAGCCTC TCAATGCAGT CCAGAAACAC AACCCATGCT	360
ATCTACTGCA GACAAGTCAT CTGATTCATC GAGTCCAGAA AGGGCATCCG CACAATCCAG	420
CACAGAAAAA TTAATCAGAC CCTCAAGTCT ACAAAGCCA TCCAACCTCG AG	472

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

GAATTCGGCC TTCATGGCCT ACACCTCTTC TTAGGGCTGT TTTTAAAC ACAATGATAT	60
TCTAAGGAAC AAGAGGTTGG CTATGGACTT TTGTATACCC ATGCCTATCA TATTCGCTA	120
AATGTTTGAT TATATAGAGA CATTCTTTG GAACCTTTGAG CTGTGTGAAG ACAACACAAA	180
CCTGGCCATT CATGGCTGAC AGAAGGTTGG CCCTAACCCT GCTCAGGCCC ACACAGATTG	240
TGTAATATTC TTTGATCTG GCTCTAGTCA GCAAAGTCTT GGTGTTGTAG GATACAGGTG	300
TCTTCATGCA TTCCATTTA TACTCGAG	328

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

GAATTCGGCC TTCATGGCCT AGAAAAAGAA AAAGTAGCTG ATGAAGATGA TGTGGACAAT	60
GAGGAGGCTG CACTGCTGCA TGAAGAGGCT ACCATGACTA TTGAAGAGCT GCTGACACGC	120
TACGGGCAGA ACTGTCAAA GGGCCCTCCC CACAGCAAT CTGGAGGTGG GACAGGCGAG	180
GAACCAGGT CCCAGGGCCT CAATGGGGAG GCAGGACCTG AGGACTCAAC TAGGGAACT	240
CCTTCACAAG AAAATGGCCC CACAGCCAAG GCCTACACAG GCTTTTCCTC CAACTCGGAA	300
CGTGGAAGCTC GAG	313

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

GAATTCGGCT TCATGGCCTA GCGTTGTGTG CATGCGAGCG CTCCTGCAGG CGTGTGCATG	60
GGGCCAGGTG TGCACGTGGA TGCCCGGGTG AGTGTGTGTG CATGCACGTG TGTGCACGCA	120

TGTGCACATG CCTCCAGCCC CACCTTCCAA CCCCTCAGTG CCCCCAGGAC AGGGGCCCCCT	180
CTTAGCTATC AGGGTATGGC CGGACCGGCC CTTCCTGCCC AGCANGTTGC AAGCACTTGG	240
CCAGGCCGGC CCTCCAGGNT GCTGCTGCGT GGGGGCCCCG GTGCCCCCAG GTCCATGCAG	300
ACTGGGGATT CGGTGGGGAG GGGCGCTTCT AAGGAACCAA ACTGACGCTC ACTCTGGGCT	360
TCCAAGCAC CCTTAGCACG GAGCCACCC CTAGCTCGAG	400

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

GAATTCGGCC TTCATGGCCT ACCCACCCTG TAGTCAACCC CACTCGTACT GTAGCGAGAC	60
AAAAACATGC CATTGTGAAG AAGGGTACAC TGAAGTCATG TCTTCTAACA GCACCCCTGA	120
GCAATGCACA CTTATCCCCG TGGTGGTATT ACCCACCATG GAGGACAAAA GAGGAGATGT	180
GAAAACCAAGT CGGGCTGTAC ATCCAACCCA ACCCTCCAGT AACCCAGCAG GACGGGGGAG	240
GACCTGGTTT CTACAGCCAT TTGGGCCAGA TGGGAGACTA AAGACCTGGG TTTACGGTGT	300
AGCAGCTGGG GCATTGTGT TACTCATCTT TATTGTCTCC ATGATTATC TAGCTTGCAA	360
AAAGCCAAAG AAACCCCCCT GCCTCGAG	388

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

GAATTCGGCC AAAGAGGCCT AATTGAATTC TAGACCTGCG TCGACCGAAC CGAGTTGTAC	60
ATTTTTTTTG TGATGGGTTA TTTTATTATT TAATTATAT TGTGTTTTG GTTTTTTTTT	120
GGTTGGTTTT NGATTTATGA CAATNCCACT CTTGGCCCCA GTTGTCGTCC TGCTACTCCC	180
TCCCCTGTCC ATCACCCTGG CTCCCAGACC AGGCTCAGCA ACACATTGAG TCTTGGGTTC	240
CAGGAACCTT GCCAACCTCA ACCCTCCAGC CCGTGCTCCA CTGGCTATGG CTCAGACCAA	300
GGGCTCCTCC TCTCCNTCT TGCCCTATGG AACAGCCCGG GTGCTCCAAG GGGGCCAGGA	360
GGGCATGGCT TGGCTCCCAA GATAAGGGGT CCGGGGCCAG GACACCCAGG CAAGGTGGCC	420
CCTCCCTGCC TAGCCCCCTT CCCCCACCC AAAGTCGAG	459

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

GAATTCGGCC TTCATGGCCT ACAACCTGGA AAATTCTCTG ACTTAGAAAT TTAAACAAAA	60
CCCTCCCCTT TCATTGAATC TCCATTGTCT GGAGTTTGCT TGTTTTAATC TAGCCTGTTC	120
CTCCACTATG GGCTCCCTTT CAACTATGC CCTGCTTCAA CTAACCCCTA CTGCTTTTTT	180
GACAATTCTA GTACAACCTC AGCACCTGCT TGCTCCAGTT TTCCGGACAC TATCTATCTT	240
GACTAATCAG TCTAATTGCT GGTATGTGA ACATCTAGAT AATGCAGAAC AACCCGAACA	300
CCTCGAG	307

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

GAATTCGGCC TTCATGGCCT ACCAATACTA AGCTTATTTT ATTGTAATAC AGTTATTTGT	60
ACCACCTTAG AGCAATCTTT TGAAGAACAA GAAACACATA TTGAGCCACC ACGCCAGCC	120
TTTTTTCAGT TTATTTTAA TCTTTTGCTG TTCATTGGCT CATCTGTGT ATAAGCATGT	180
TAAATTTACC CAAATATGAA AATAGCCTCC CCTTGGCCCT GAACTCCTCT ACAAGCAACT	240
ACCTCATGAT TTTATCTCTT TATCCTCAA TTCTTTGGAA TATAATTTAT ACTTGTTTCA	300
TCCCTACCAC CCTCGAG	317

(2) INFORMATION FOR SEQ ID NO:528:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:

GAATTCGGCC TTCATGGCCT ACAGCAGTGT GCTTTCATCC AGTTTGCCAC ACGGCAGGCT	60
GCAGAAGTGG CTGTGAGAAG TCCTTTAATA AGTNGATTGT AAATGGCCGC AGACTGTATG	120
TGAAATGGGG AAGATCCAG GCAGCCAGAG GAAAAGAAAA AGAGAAGGAT GGNACTACAG	180
ACTCTGGGAT CAACTAGAA CCTGTTCCAG GATTGCCAGG AGCTCTTCCT CCTCCTCCTG	240
CAGCAGAAGA AGAAGCCTCT GCCAACTACT TCAACTTGCC CCCAAGTGGT CCTCCAGCTG	300
TGGTGAACAT TGATNTGCCA CCGCCCCNTG GCATTGCTNC ACCCCCACCC CCAGNTTTTG	360
GGCCACACAT GTTNCACCA ATGGGACCAC CCCCTNNNAC TCGAG	405

(2) INFORMATION FOR SEQ ID NO:529:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:

GAATTCGGCC TTCATGGCCT AAGAAACCAA ATTAGCAGAC GGATAGAATA TAAAGCAAGA	60
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GGCAATACTT ATAGTGTATT AAGAACTTG CTAGACCCCA TCCAAATTAC TCAGTCTACT	120
GTTGGTTGAT AGAATTACTT TAGGAAGAGT ACGTTTTTGC CTTGGAAATA CACTGGAAGT	180
GGTACCAAAC AAATCTAATA AAATGATGTT AAAGAGATTT GCAGTAATTT TTATCAACTT	240
TCAGTTTGCA AACTTTTATA AAGATATGAA CGGGACACTC GAG	283

(2) INFORMATION FOR SEQ ID NO:530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:530:

GAATTCGGCC TTCATGGCCT TTCTATAAAT GAGTTCTTTA TAAGAAGCTT GTATCATTCT	60
CACAAATTAA AAATAATAAT ATTTTAGCAA GCTATTTTTT AAATATAATT TAAGCCCACA	120
CTTCCACATT TGGGGTAAGT GATAATTTTT TCCTCTGAAA GACAACAAAT ACTAACACAG	180
GCCCAGACTT GGCTTTTGTG AGTCAATTAG TGATCCGAAG GTGAGTGGTA TTTAAACGTA	240
TGATGAGGGT AAGATTTGAT TTATTTTACA TATATATCTT CTGGTATCTG TGTGTGTGTG	300
TGTGTGGTGT GAAGCTCGAG	320

(2) INFORMATION FOR SEQ ID NO:531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:

GAATTCGGCT TCATGGCTTG GGGGTGACAG TTAATATATN CGGTCATTTT AGATTGCTTC	60
CACTAATATT GGTATTATCCA TATTATAAAA TATTTTAGTG AGTATAAAAT TGTCTGCATT	120
CATAAAGATG CATAAAATTA ACTACAGAAC CAGCTTGAGT AATGCTTTTC TCTTCTTTTC	180
TTCTTGTCAA TCAGATATTA TCTTTATACA TTGTTTTAGA GTATACATCT ATCAAAATGC	240
AACATTGTTG AAGGATATGT AATTTATACA GCAAACGTGT AATGGATAAA AATGTGCAAA	300
AACAATCCTT AAAGTATTGT ATTTGAACNA AAACAATCTT AAACCACATA ATCTGAAAAA	360
AAGGGGTACA TATTTTACCA AATATACTAA TCCATACAAG ACTGCTTGAG AAAAAGAATA	420
TGCCACCTAC TCGAG	435

(2) INFORMATION FOR SEQ ID NO:532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:

GAATTCGGCC TTCATGGCCT AAGCCATCAG ATTGAAATTA ATTTAGACAG GAAGAATCTA	60
TATAAATTTG ATGCATAGCA AACTCTGACA TAATTTGGTT TATTTTGAAG TCTGGCATAT	120

TTTTCATCAC TTTTATTTT ACGGGTAAAT CATAATATAT CATATTTTCA ATAAAAGTAT	180
TTTCTTAAAA ATCTGCCATT TGCTTCACAG ATTTTAAATC TTCTAACAGA AAAAGAAGTA	240
AATATTGTTT TGCCAACACA GTCCATTGTT CCAAGAACTT TTGTGCTTAA ACCAGGAATG	300
GTTCTGTTTT TGGGTGCTAT AGGCCGCATA GCCCTCGAG	339

(2) INFORMATION FOR SEQ ID NO:533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:

GAATTCGGCC TTCATGGCCT AATGTGCTCC AGGAGGCGCT GGGGGATGGT GACCTCCCAA	60
GGCGGGCAGA NGACTTCTGC CGTCAGGGTC GCCTGCTGCT GAGCCTGGGG GATGAGGCGG	120
CGGCCGCAGG GTCTGGATCC CCTGTGCCGT CGCTCTTCC TTTTTCGACG CCTCCGCCGC	180
CGCCTGAGGA GCGGAGCTAG CCGGGAGTTA CACCGCCACC GCCAGGATGG ATAGAATGAC	240
AGAAGATGCT CTTGCTTGA ATCTGTTGAA GCGGAGCTTG GACCCAGCAG ATGAGCGAGA	300
TGATGTCCTG GCAAAGCGAC TCAAATGGA GGGGCATGAG GCCATGGAAC GTCTGAAAT	360
GTTGGCATTG CTCNAAAGGA AGGANTTGGC AAATCTTGAG GTGCCACATG ANTTACCCAC	420
CNAACAGGAT GGCAGTGGTG TCAAGGGCCA TGAAGAAAAA CTTAACGGGA ACAACTCGAG	480

(2) INFORMATION FOR SEQ ID NO:534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:

GAATTCGGCC TTCATGGCCT ATATGATTTT TTAATCTATG ATGGTTTATG TGAATAGGAT	60
TTTCTCAGTT GTCAGCCTGG GCGACAGAGC GATACTCCAT CTAAAAA AAAA	120
GAGGTGACTA GGCCATGAAG GCTCTGTCCT CACAGATGGA TTAATGCCAT TGTGTGGGA	180
GTGGTTTTCT CATTGAAGGA TGAGCTTGAG CTTGGCCCCC TTCCTTCTCC CGCCTCATTC	240
CCCTCTATGT NGCCCCTATG ATGCCTAANG CCATGTTATG ATGTGGCAAA AAGGCCCTCG	300
CCAGATGCCA GCCCCTTGAC CNTGGAATTC CCAGCATCNA GAACTGTGGA CCNAATGNAT	360
GTTTTTTCCT TATAAANTAA CCNGCCACNG GTATTTTGT AAAGCNGCAC CNAGCAGACT	420
CGAG	424

(2) INFORMATION FOR SEQ ID NO:535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:

GAATTCGGCC	TTCATGGCCT	ACGTTGACTT	AATCAGAGGG	TCAACATTG	CCAAAGCAAA	60
ACCTGAAATT	CCATGGACAT	CTCTGACTCG	GAAGGGGCTT	GTTCGAGTTG	TATTTTTC	120
ATTGTTGAGC	AATTGGTGGA	TTCAGGTAC	CTCTTAAGA	ATCTTGTTT	GGCTGTTACT	180
ACTTTATTTT	ATGCAAGTTA	TAGCAATTGT	CTTATATTG	ATGATGCCTA	TTGTGAACAT	240
AAGTGAAGTA	CTTGGACCCT	TGTGCCTTAT	GCTACTCATG	GGAACGTGCC	ACTGTCNAAT	300
TGTGTCTACT	CAGATAACAA	GACNTCAGG	AAACCTCGAG			340

(2) INFORMATION FOR SEQ ID NO:536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:

GAATTCGGCC	TTCATGGCCT	AGGCGCTCGC	TGAGGCAAAA	GGAGGCGCTC	GGCCCGCGGC	60
CTGACAGGGA	CTTAGCCCGC	AGAGATCGAC	CCCGCGCGCG	TGACCCACAC	CCCACCCACT	120
CATCCATCTA	TCCACTCCCT	GCGCCGCCCT	CTCCACCCCT	GAGCAGAGCC	CCCGAGGATG	180
ATAAACACCC	AGGACAGTAT	TTTGCCTTTG	AGTAACTGTC	CCCAGCTCCA	GTGCTGCAGG	240
CACATTGTTC	CAGGGCCTCT	GTGGTGCTCC	TGATGCCCCT	CACCCACTGT	CGAAGATCCC	300
CGGTGGGCGA	GGGGGCGGCA	GGGATCCTTC	TCTCTCAGCT	CTAATATATA	AGGACGAGAA	360
GCTCACTGTG	ACCCAGGACC	TCCCTGTGAA	TGATGGAAAA	CCTCACATCG	TCCACTTCCA	420
GTATGAGGTC	ACCGAGGGTA	CTCGAG				446

(2) INFORMATION FOR SEQ ID NO:537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:

GGCAAATTAC	ATCACCAAAT	CAGCATATTC	TCCACTGGAA	AGGAGAGGCC	CACATAGCCA	60
AATTATAATC	TGCAGGTTTC	TGAGCCAGTG	TTAAATCTGA	ACAGAGAAAA	GATTTTTC	120
TCAATTGGCA	AATTTTAATG	ACATCACTCA	TTGATACCCC	AAAATCTCCA	GTTCTTACCA	180
AGCTTGGCCT	TGCCAGTGG	TTCCTCTGTT	CCCTCAACAA	TGTTTCATGG	NATCTAACAA	240
CTTCCCTACC	CATAACCTT	CTCAGCTTTC	ATGGTGAACC	AAGCCTCCTC	TGTCGCACTA	300
ACCTTCCCAG	CTTTCATGGT	GAACCAAGCC	TCCTCTGTCC	CGCTATTCTC	GAG	353

(2) INFORMATION FOR SEQ ID NO:538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:

GAATTCGGCC TTCATGGCCT AAGAAGGAGN AGCAAGCGGA TTTCAGAGAG GTTGTTCCTC	60
AGAAAAAAT GGTATTCTTCT TTGAACTCAT GCCTGAGCTT TATTGTTTA TTGTTATGCC	120
ACTGGATTGG GACAGCATCA CCTCTGAATC TTGAAGACCC TAATGTGTGT AGCCACTGGG	180
AAAGCTACTC AGTGACTGTG CAAGAGTCAT ACCCACATCC CTTACTCGAG	230

(2) INFORMATION FOR SEQ ID NO:539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:

GNAAACCAGA GATCCCCATA GATGGAACAG AATTATCCCA CTACCGTCAG CGTGCCCTCC	60
TGCAATCACA GCCAGTTCGC CGGACGCCTC TCCTCCACAA TTTCTGCAC ATGCTGTCCT	120
CCCGCTCTTC TGGCATCCAG GTGGGAGAGC AAAGCACAGT GCAAGATTCT GNTACCCCTT	180
CACCCCCACC GCCTCCCCCT CAGCCCTCCA CGGAGCGCCC CAGGACTTCC GCTTACATCA	240
GGCTCCGACA CGGGTCAGT TACCCACAG CTGAGTGCTG CCAGCACCTT GGGATCCTGT	300
GCCTTTGCAG CCGCTGCTCT GGCACCTCGAG	330

(2) INFORMATION FOR SEQ ID NO:540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:540:

GAATTCGGCC TTCATGGCCT ACTCCGACTT TCGTCTTGA TTAATGAAAA CATTCTTGGC	60
AAATGCTTTC GCTCTGGTCC GTCTTGCGCC GGTCCAAGAA TTTCACCTAG TTACCCCTCTA	120
GAATTATTGC ATTGGGGCCA GGTGGTGTCT AGTACAGTTT TTTACTTTGG AGAATTTATT	180
GAAATTTTCT TTGGCTGAGA ATGCCCTCAG TGTTTGTGGT TATTCCTTGG ATACTTGCAA	240
ATCGATTGTA TTTTCTCTGG GACACGGGGT TTCAGATAGA TCAGTTAAAT GAAGCTTGAT	300
TATATCGTAT TTCACGTCGC ATGCCATGTG TCTTGTCTGT TGGACTGTCA GGTCTCAAGA	360
GACGGGCTTG GGTTCCTCTG TGTGGCTGCT GCCTTGCCCC TTCCCCGATC CACACTCGAG	420

(2) INFORMATION FOR SEQ ID NO:541:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:

GTGGGCAAAG AAATGAAGTA CATTAAAGGAG GCCTTTTTTT TCCTCCAATG GCTGTTAGAT	60
TGTGTATTGC AACCAGGAGT TGTCAAGCTC CTGATCCTAA TCCAAGCTGG GGAAGTGTGT	120
ACAGTGTGGC CAGCTGCCTT GCCAGCTGCC TTACCAGGCA GGTCTCGCAT CTGCCATTGT	180

CATCCCATTG GAATCAAGTT GCAAGCCAGT GAACTTGCTG GGGTGTGCCC AGGTCAGAAC	240
AGTTACAGCT TAAAAGCCTT TGCTGCCCTT TTTCAGATCC TGTTCCCTGGG AGAGTCTCCC	300
ACACTAAGTT CAGTGTGGGT ACCAGCTGTG GTGAGGGTGT GCTGCCACTG CAGCTGCTGT	360
CTGGGCATCT GTGTTAGGGC CAATACTTCA AGAAGTGTGA GTCATTGTGA AGTGACTGTA	420
GGCAGCTGGG AAATAACAGC TGTGAACAGA GAACAACG AG	462

(2) INFORMATION FOR SEQ ID NO:542:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:

GAATTCGGCC TTCATGGCCT ATGGGAGATA GGGGACTTAA TTATTTGTG GGTTTTTTCT	60
TTTTTAGGTC TTAGGAAGGT CTTTGTTCCTA TAGGTATCTG TATAATACAA TTTTATTAGG	120
TGTAATAGAG ACAGTTTTGT GGAAACAGAA TGCTGACACT GATTAAATTT AAGGTGTATA	180
TATGTTTAGT CTTTGAGATG ATCTGTATGC TACATGTAGG TGTACATTGT AATTTTCTGG	240
CTTGTAATTT TTTGTATCAT ACTCTGTTTC GGGAAATTGC AAATGCCTAT GACCAGCCTA	300
TGACATCTGA ACCATACCAA CTGACCTTAG AAACAACGAC ACTCGAG	347

(2) INFORMATION FOR SEQ ID NO:543:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:

GAATTCGGCC GCCTAGCAAA AGTGAAAAA TAAATAAAAC AAGCCACAGA TTGGGACAAA	60
ATATTTGTGA AGGATATATC TGATTAAGAA GTTATATCCA GAATATATGA AGAACTTTCA	120
AAACTAAAGA AAACAATTCA TTTTCTTAAT TGGGCAAAAG ATTTAAACAA ATATTTTACT	180
AAAGAAGATA TCCAGATAGC AAATAAACAC ATGATATTCA CCGAAATTAT TAATTAGGAA	240
AATGCAAATT AAGATGAATA TCATTATATA CCTACTAGAA TGGCTATATT TTAAAAGTTT	300
GACACTGCCA ATTACTGGTA AAGATGCAAA TCAGCGGAAG CTCGAG	346

(2) INFORMATION FOR SEQ ID NO:544:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:

GAATTCGGCC TTCATGGCCT ACTTTCTTCC TACATTAGTG GCATACTCTG AATGACCTAG	60
TGAACAGACT GAGAAGAGGC CTCTGAATTG CAGAGTCTCG TCTGTAGGAG AAGGTTTCAGG	120
AGAGTATTGA ATTTTAGGGA CTAGAATCCA TCTTACCTAT GCTGTTGCAA TCGCATGCTG	180

ACTGGAAGTG TGGGAAAGAG ACTTACAAGT AAGGACATGG GTTTGTTTTG TTTTGTGTTT	240
TTTGTGACAG AGTGAGACCC TGTCTCGNAA AAGGAAAAAA AGTAATAGAA CATTAAATAC	300
AGTATCACAC CATTATGGT TAAAAAGNA AAAAGACAAG ACACATATG AAGTGAGTGT	360
CTTTTAAAGT TAAAAAATT AAATGAAAAC AAACCTCGAG	399

(2) INFORMATION FOR SEQ ID NO:545:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 367 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:

GAATTCGGCC GCCTCCATCT CCCTGGCCAT GTTCTTCTTG AAGACCCTGA CAGTGGCTTC	60
TTCTTTGTGG CAGCTGGCCA ACAGCCAGAC CCTGACAGCC AGCCCCAAG CACCTGGGTC	120
CCCAGAGGAT TCTGAGGGTG TCCCCCTCAT CAGCCTGCCC CGCGTGCCAC AGGGAGGGAG	180
TCAGCCTGGG CCCAGCCGGG GATTAAGTCT CATGTCCAGT CAGGGCAGTG TGGACTCAGA	240
CCACCTAGGT TATGATGGTG GCAGCAGTGG CTCAGACAGT GAGGGTCCCA ATGACACCCT	300
TGGTGAGAAG GCCCCCTTCA CATTGCGGAC TCCACCTGGG CCAGCACCTC CACAGACTTC	360
ACTCGAG	367

(2) INFORMATION FOR SEQ ID NO:546:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:

GAATTCGGCC AAAGAGGCCT AACCGCGGNC GCTCTACAAC TAGTGGATCC CCCGGGCTGC	60
AGGAATTCTGA TATCAAGCTT AATTAAGAAT TCGGCCAAAG AGGCCTAAGC GAGAAGAGTC	120
CCCGCTCCGT GCCCTACCAC TACTTTGAGA AGGGCCGGCT AGATGAGTGT CAGATGTACC	180
GTTTGCATGA GCAGGCTCCA AGGAGCGCCC ATCGCTTCAT TACCGAGAAC CCTGTGTTCT	240
CCCGCTGGGC CAAGAAGCGA CCCATCGTGT TCGCCACCC GTCCTGGAGG GCCAAGTAGT	300
TCCTGTTGCC AGTGAAGTCC AGGCCTCAGC CAGGCCTGTG ACCCATTCCTA GGCCAACACG	360
GCTCTAATGT GAGCATTAT GACTCACCTT CTACCTGACA CCAGGTAGAA CATGAAGTCT	420
CTATTACCCA AACTGGGTA CACTCGGAGG TCGAG	455

(2) INFORMATION FOR SEQ ID NO:547:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 401 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

GAATTCGGCC TTCATGGCCT AGTCATTTTG TCAGCTTTCA CACAAGAATC TTTGATCCTA	60
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TTGTAATAGT TAATAAGGAA GTTCTTCTCT TGCTCAAAGA AGTCATCTAC CTCCTTAACT	120
CCAGTAAAAA GGACTTCATC AGCACTTTTC ACCACACTTT TGAAGAAGCC ACCAAACATT	180
TCTTTAGTAT TTTTCCGCCT AACACTTAGA TCCTGATCAT ATTCCAGGAA AACATGAAAG	240
TTGCGATCTT TACTGAGAAC AGGGTGAGAA GAAAGCCGCT GAAGAAAGAC TTCATGGGAG	300
GACACAGTCT TCTTAAACAC AGCGAGATAC TCAGCTTCCA GTTCTTGTTT CATCTGGGCT	360
TATTATTCCA CCTTCTCCA GTTCTGTCAT CTTCTCTCGA G	401

(2) INFORMATION FOR SEQ ID NO:548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:

GAATTCGGCC TTCATGGCCT ACAAGCCCCT CTTACCTCTC TGGATGCTTT CTTTAACT	60
AACTCACCAC TGTGCTTCCC TGCAGACACC CAGAGCTCAG GACTGGGCAA GGCCAGGGA	120
TTCTACCCC TTCCCAGCT GGGAGGAGCT TGCCTGCCTG GCCACAGACA GTGTATCTTC	180
TAATTGGCTA AGTGGGCCTT GCCCAGAGTC CAGCTGTGTG GCTTTTATCA TGCATGACAA	240
ACCCCTGGCT TTCCTGCCAG ATGGTAGGAC ATGGACCTTG ACCTGGGAAA GCCATTACTC	300
TTGTGTCTGC TACTGCCCTC CCACAGTCAC CCCAATATTA CAAGCACTGC CCCATTGGCT	360
CGAG	364

(2) INFORMATION FOR SEQ ID NO:549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:

GAATTCGGCC AAAGAGGCCT ATGCTTTTCT TTGCAGCACT TAGCACAAAT AGTAATTTT	60
ATTTTACTTT TATAGATGTA TTTTATGTCC CTCCACCAGA CTGTATACTC CATGAGGACA	120
AGGATATTGA TGTTATGTT AACTCTTGTA CACTCAGTGC CTGGCACCAT GCCTGACCCA	180
GAAGAGGGAC TCGAG	195

(2) INFORMATION FOR SEQ ID NO:550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550:

GAATTCGGCC AAAGAGGCCT AACATAATGC GCTAGCAGAC TTGGGAATTA GGGGAGAAT	60
GCTGCTCTAA ATTCAGGAAA TCATGGCACG GTTTCATATT GAACATGGTC TATTCCTACC	120
ACTAGCGCTT TCCTGGCTGA TTTCTTCTCC AGCTGGAGAC TTCTTTCTGG TTTTCCAAT	180

TATGCTCCAC CCTCACCCCA ACCCACCCAT AAACCACTGG CTGCCGGAAG CAGTATCTTT	240
CATAGTGGTG AGTTCTGGAT TTTCAAGCAGT AATGGCCGAG AGTCAGGGAC CAGATGAGTG	300
TGTGTGAGCT GGTGAGAAAA GGTAGATTCC CTCGA	335

(2) INFORMATION FOR SEQ ID NO:551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:

GCCAAACATG TCTCACCNA NCCCAATGT CCCCNGGGGG AGCAAAATCT CCCCTGGACA	60
ACTGTGGAAT CACTGTNNGG AAGTGTTTAC TTGAGTGGTT TNCTGGCCTG GGCCTCATAC	120
TCTGAATTTT TGAAGTAAAT GGTCTGGGGG TGCTGGGGGT GGAGAGCAGA GCACTGGTAT	180
TTTAGGAGA TCCCCCTGTC ATTCTAAAGC ATATCCAGGG TTAAGCACCA TTAATCTGAN	240
GATCTNCNGT CTGATCTGCG GGCCCCCTTT CATCTANGTG CAGTATTTTT CTCTATGCTT	300
TTTAAAATAA TGAAAGTTTC TNGAACTCCA TCTGGACTTG AAATATAGCC TGCCACACAG	360
TTAGCAAATA TAGCAAGAAT AACAAAGTGT CTAAATGGAT TTTTAATTTA TTATGGCAAT	420
AGTACATTCC AANAGGGTGG CATTTTTTAA AATGAGATT TTCTTTTGGG CCTAAGATTA	480
CAGTCACATG GTTCCAAATT CAGAGGGTTC AAAAGGACAC AGAAAAGCCT GCTTCCCACT	540
TGNGCCCACT GGCCTCCCTT TTTTTCGCAT AAATGGCAGT ATATAGCTTT GTCTGTTCTT	600
TGTTTNNNGA GCTTAATACC TTAGAGACAG ATTTNGTAT ATCTGTACCT ACAGAACTCG	660
AG	662

(2) INFORMATION FOR SEQ ID NO:552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:

GCTGTTTTAA AAGAGTTGGG GGAAGAGGTA GAAATGAATC TTTTGGTTTA GTTTTTTAAT	60
TCTCTAAGGA CAACATTGGG GAAGTGAGCT TTAGAGTTAT ATTTGCAGTA TTTATTTTAA	120
TCATGAAATA TTCAAGTCTA GGCCCTTGGT GAATTGAGGC CTGGTGAGTA TTTCTGCTTT	180
CCCCCTGGAG AGATTGAGAT GGTCTCTGAT TGGGAGCTTT AATTCTGTGG GCATTTGTGG	240
GACTTACCAA AGAGGTATCT AGAGTTCCTT TAAAACCCCT GCCCTGTCCC TGCCACAAAA	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:553:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:

GTCAAAAGAG	GAGCTAGGAC	CAGATCTCTA	AGTCTTACNG	TCCAGGTCAA	AAAACAAGTA	60
CTTTCCTATC	TGGTTATACA	GAAATCTGGA	AACAGTCACT	CCCAGCCTCA	CAATTAAAAA	120
AACCTGGACA	TACAGAAAGT	TCATAGTTTT	CCTTGAACTC	ATGATAGTGC	TGAGATTTC	180
CGGCAACCAA	CTGGCCCAGA	TACTCCAGAG	TCAAAGACAC	TGTAAGGAGA	GTTGACATNT	240
GAGCATTAGA	CAAGACACAG	ATGGTANGAG	TTAAGCTAGG	GTTACTCGAG		290

(2) INFORMATION FOR SEQ ID NO:554:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:

GAATTCGGCC	TTCATGGCCT	ACTCTATGGG	GATGAGGTAG	AGGAGAGCAA	GATATTTCGG	60
CAGCAGGGAA	AAGGGTAGAA	CAGAATAGGG	TGACACAATT	TACACTTGAT	ACTGCATTAA	120
CATCTGGTAG	AGTGTCTAGG	GCAAAGGTTA	GCCAAAATAT	AGCTGGATGG	TTGAGGGATT	180
TAGAAGGAGT	TGGGATGAAT	CCATAGTCTC	AATGAATGGA	GAAAAAGTAA	CTCAGGAAAG	240
TAAATGCTGG	TGACTTATCA	GCGGGTGGCT	GGTGATGTTT	GGTTTGGATT	GTGAAAGCTG	300
CTTAGACCAA	GATGGCTGA	GGGAAGGGGA	GGAGAGTGAG	CATGTAGAGG	TTGAGGCACT	360
TGGTCTCGAG						370

(2) INFORMATION FOR SEQ ID NO:555:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:

GAATTCGGCC	AAAGAGGCCT	AATTGCCAAT	CAACAACCTT	TCCTAATCCA	CCTTGATCCT	60
CAATCATAAT	ACTCAAAAAC	TGCCAAAAAC	AAAATCTTCC	TGACAAAAAT	ACAGGCCAAA	120
CTTCCTCATC	TGCTTTCCAG	GTCTTCTGTA	ATCTTATCCC	AGCTTATTTA	CAGTCTCTCA	180
TTTACTAAGA	AAACCCAAA	TAATCTTTC	CTGCCCCAAA	TTCATGTTCT	TCCCTTTTCT	240
TTTGTTTATA	CTACCATACA	TATCTAGAAA	TGATACTCAA	ATATTTCATC	TCAGCACCT	300
CGAG						304

(2) INFORMATION FOR SEQ ID NO:556:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:

GAATTCGGCC	TTCATGGCCT	AGAGGGGAAA	GCATATCACT	AGGACTGTGA	CCCCTGTGCC	60
TACCCATCTT	ACTCTCTACC	TCTTAGGAAA	GTTTCACTGT	GTTTACTTGG	GACTTCTGGA	120

CTAGCTGCCG	TTTGCAACAG	TGGACTTACC	AGTTTGCCAC	TACTCTGCTA	CCTTTCTACT	180
GGTGCACACA	CCTTAGTAAG	GCAGTTTGAT	TACTAAATGC	AGCTGTCTCC	AGAAATGGAA	240
TGATGCTATA	GGCCACTTAC	TAAATGAATG	ATCAGGAGTC	TCGAG		285

(2) INFORMATION FOR SEQ ID NO:557:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:

GAATTCGGCC	TTCATGGCCT	AGCTGGATCT	GCCCACTGTG	CACTCCATCA	TCAGCAAAAT	60
GATCATTAAT	GAGGAGCTGA	TGGCCTCCCT	GGACCAGCCA	ACACAGACAG	TGGTGATGCA	120
CCGCACTGAG	CCCACTGCCC	AGCAGAACCT	GGCTCTGCAG	CTGGCCGAGA	AGCTGGGCAG	180
CCTGGTGGAG	AACAACGAAC	GGGTGTTTGA	CCACAAGCAG	GGCACCTACG	GGGGCTACTT	240
CCGAGACCAG	AAGGACGGCT	ACCGCAAAAA	CGAGGGCTAC	ATGCGCCGCG	GTGGCTACCG	300
CCAGCAGCAG	TCTCAGACGG	CCTACTGAGC	TCTCCACTCT	GTTTCCCGCC	TGGGCCATCC	360
AACCTTGAAG	TCCTAAACCA	CACCTCAGTC	ACTAAAGGTC	TGTCTCGAG		409

(2) INFORMATION FOR SEQ ID NO:558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:558:

GAATTCGGCC	TTCATGGCCT	AGGAAAAAGA	GATATAAAAA	AAAGAAAAAG	AGGNGGTACC	60
AGCCAACAGG	AAGACCACGG	GGAAGACCAG	AAGGAAGGAG	AAATCCTATA	TACTACTATA	120
TAGATAAGAA	GAAACAATTT	AGAAGCAGAG	GATCTGGCTT	CCCATTTTTA	GAATCAGAGA	180
ATGAAAAAAA	CGCACCTTGG	AGAAAAATTT	TAACGTTTGA	GCAAGCTGTT	GCAAGAGGAT	240
TTTTTAACTA	TATTGAAAAA	CTGAAGTATG	AACACCACCG	TCTCGAG		287

(2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

GAATTCGGCC	TTCATGGCCT	ACTTCTCAAA	AATAGATGTA	CTTGACTACT	CTTTTCTTGA	60
TTCTTCTGGG	AGTAACCATC	TCTTTGGAGA	TGTTTGTAG	TAAGGTTATA	AAAATAACCT	120
TACTGAGGAA	CTCCCATGCA	ATCCTCTGAA	AATAATAAAA	ATTTCCTTAT	TTCAAGAACT	180
CTTATTTAAC	AAAGTAATTG	TAGGGTGA	ATACTCTAGG	GGCAAATGAT	TTATTGTGCC	240
TTTTGTAAAA	GTCAACACTT	GGCAGGTGTG	TGTTTGACAC	TGGCTGATGC	TGGGCTTATT	300

TCTCTAAGAG TATGGTAATT CTAGTAAAGT AAAGAAAATT GTTTATCAGA TATTAGGAAC 360
 TGTACATAGG CCCCCTCGAG 380

(2) INFORMATION FOR SEQ ID NO:560:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:

GAATTCGGCC TTCATGGCCT AAAATTGTTC ACGAGGGATT ACGTGGTTTA CTGTCTGTT 60
 GTCCAGATAG CTTTATATTC TTTAAGATTC AGCTCGGATT CTTATCCTAT TTTTGCCATT 120
 AACTTTCATT ATGATTTTGG CAAAGCCATT TTGTTTGCTT ACATTTTCA CTTTAAATGT 180
 GGTGTCTGGC CTCCCCCA CACTCGAG 208

(2) INFORMATION FOR SEQ ID NO:561:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 505 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:

GAATTCGGCC TTCATGGCCT ACAAACANTT TTTACTGNCT TATAAATAAA AACAGCGACA 60
 CATCCTAAAT GTGCACCTGT GCCGTGGCTG AGCCGCTGCA GTGAGGGCTA GTGTGCAACA 120
 CCGATGCTGT GCTGGACGCG TGCCAGCCG GGTCCCTGA CAGGAGGCAN CCGGGGCCGG 180
 TCGTGTGTT TGCATGTTGC AGTCATGGGG CGGGNCGGC AGANGCCTGT GTGATNGTNG 240
 CGTCCCTGGA AAAAGAAGNN GGGNAGGCC CTCNCACNTG TATCCAGCC TGCAGANGGG 300
 GNGTTNTGTG GGTCTTCCC CGTGATATG CGTGTGATNT CACCCATCCC GTGTGGGTGC 360
 GCAGGAGGGG CCGAGGGAGG AGGGTGCTGG AGGGCGGAAG TTACCTCTGA CTGGAGGAGA 420
 NACCCGGCCC GTGTNACCAG CANAGGTGTG NTCGTTCTAA AACTGGGAAA AATTGTCTCT 480
 TAATTTTAAC CACAGTCCCC TCGAG 505

(2) INFORMATION FOR SEQ ID NO:562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GAATTCGGCC TTCATTAAAG AGATAAGTTA GAAAAGTCAA AGCGAGAACG GCATAACGAG 60
 ATGGAGGAGG CAGTAGGTAC AATAAAGAT AAATACGAAC GAGAAAGAGC GATGCTGTTT 120
 GATGAAAACA AGAAGCTAAC TGCTGAAAAT GAAAAGCTCT GTTCCTTTGT GGATAAACTC 180
 ACAGCTCAAA ATAGACAGCT GGAGGATGAG CTGCAGGATC TGGCAGCCAA GAAGGAGTCA 240
 GTGCCCCACT GGAAGCTCA GATTGCGGAA ATCATTCACT GGGTCAGTGA CGAGAAAGAT 300

CCCCGGGGTT ACCTTCAAGC TCTTGCTTCC NAGATGACCG AAGAGCTCGA G

351

(2) INFORMATION FOR SEQ ID NO:563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:

GAATTCGGCC TTCATGGCCT ACAAACCTGT CCATGGCATG AAAGACTTGG ACCGCCATCT	60
CAGAATCCAC ACGGGAGACA AACCGCACAA GTGTGAGTTC TGTGACAAGT GCTTCAGCCG	120
GAAGGACAAC CTGACCATGC ACATGCGGTG CCACACCACT GTGAAGCCAC ACAAGTGTCA	180
CCTGTGTGAC TACGCTGCCG TGGACAGCAG TAGCCTCAAG AAGCACCTGC GGATCCACTC	240
TGATGAGCGG CCGTACAAAT GCCAGCTCTG CCCCTATGCC AGCCGCAACT CCAGCCAGCT	300
CACCGTCCAC CTGCGATCTC ACACGGGTGA GTCCTGACC AGGGGTCTCT GAG	353

(2) INFORMATION FOR SEQ ID NO:564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:

GAATTCGGCC TTCATGGCCT ATAGAATTCC TAGACTTTAC AGACTAATAG TTTGACATCT	60
ATCTCTGGCA AAATTCGAAA CTTAAACATT AAACAAGGGA AAATGAGGGG TGGAGGNAAA	120
GACTGCGGAT TTCTAGGAAC TAACAATTG CTAAGNATCA TTCATTTTAA AACTAATGTT	180
ATTTACTTTT GTGGTAGATC AGGGNATATG CAAGATCTTT ACTTTTCAGC AAGACATTTT	240
TCTCATAATG TCCTTATGGA GAAGACTGCT CTATGGACTA GNATAGTTG ATAAGAAAGG	300
GCTGAGTCCA GCGNATTCAT TAGTTCAAGC AAAATCTACT GGAGGCCAAC TAGATTTCCA	360
GCCATTATCG TACTTGGCAC TTTCNATACT TTGAATTTA ACCACCACAC CTCGAG	416

(2) INFORMATION FOR SEQ ID NO:565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:

GAATTCGGCC TTCATGGCCT AAGACGGGGT TTCACCATGT TAGCCAGGAT GGTCTCGATC	60
TCCTGACCTC GTGATCCTCC CGCCTCAGCC TTCCGAAGTG CTGGGATTAC AGGCGTGAAC	120
CACCACGCCC AGCCATATAT CAGGAACCTG AGCATCCATG GAGTTTGGTG TCCAAGGGAG	180
GTCCTGGAAC CAATCCGCCA TGGATACTGA GGGATGACTA TAATATGAAC CTTGTATGTA	240
TGTAATTTAC CATTTTCTAG TTAGCCACAT TAAAAAAGGA AAAAGAAACA GGTGAAAAAT	300
ATTTAAAAAA TACGTTAACA CAATATATCC AGAACATGAT TTCACATTGA AATCAATATA	360

AAAATTACTG AAATAGTTTA CAGTCTGGTG TGCATTTTAG ACTTAAAGCA TATCCCTTTG 420
GGCATGGTGG CCCATGCCCTG TAGTCCTAGC CACTGAAGGC TCGAG 465

(2) INFORMATION FOR SEQ ID NO:566:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:

GAATTCGGCC TTCATGGCCT ACAGCGAGAA GGAGTGTATG AGTGTGAGTG TGTGTGCATG 60
 GAAGTTGGGC ACTGGGCGTC TGANTCCTTC CCCACCCAAG AGAGGAAGGA CCCCTCACCA 120
 CCCCCACTGG CGAGACAGTT TACTTTGCCG ACTTGCCATG TTTTGGCCAA AACCAAGATT 180
 TTGAAGGAAA TGAGTGGCCA GCGCCAGGGC CCAGGCCATG TGGCCTGCCC AGCCTCAATG 240
 TNACTTGGTG GCGGGGTGGG GTGGGGGTGG GCAGCAGCAT CCCAGCCTTG AGATGCTTCA 300
 CTTTCCTTCT CTGTAACCAG ACTTTGAAAA ATTGTTCTGT TCATCAGGCA TCTCGAG 357

(2) INFORMATION FOR SEQ ID NO:567:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:

GAATTCGGCC TTCATGGCCT ATCTGCACTG AATTAGAACA AAATTTAGGA GACTTCTAAT 60
 TTGAAGCCAG AGGTGCTGAC TTTTGAGTCT TTGGAGATTG CCTGTTGGAA ATATTCCTGT 120
 TGAGGGCCAA TGTCCCAATG GGCTCTGAAG ATGAGAAGGA TCCCTGCCCT ATGTGGATGC 180
 CACTGGATCT GGAATCATTT CTGTGGCTCA GATTTCTGTA CACATTCTGC CAGGACAGGA 240
 GCAGCCGTAT TGGGAAAAGA AGGGGGACAA TAACTAGAAA CGAACTAAGA TGTGGCCCTT 300
 GCTTTTGTA TTTTAATTTA ATGGGAAACA CTCGAG 336

(2) INFORMATION FOR SEQ ID NO:568:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:

GAATTCGGCC TTCATGGNCT ACCTGGACCT TGGGTGGCAG GCCTGGGGCC TTCAGTCTCT 60
 AATTCAGGAG GTAGCCAGTC GCTGGAACTA AGANTGAACT TCAGCTGTTG TTGCCATAGC 120
 TGGAGGGAAG AGGGAAAGGA GCGCTGCAGG GGAGCAGAGA CCTCACCTT CCTCTGCCGA 180
 CATCAGGCTG CCGGTGCTGG ACGGGGCCCT GGCAACCGTG GCAGGAGTGG TGATGTCCGA 240
 TGATGGTAAC AAGGGCTTCC TGAGGACCCC GAGCTGTCTT AAGGGCTCTT TACCTGGAGT 300
 AAGTATCCCC TTTAATCCTC CCAACAACAC TGTGAAATTG ATTCTGTTGT TATTCCTATT 360

TCACCGATGA GGAACCCACA GCCCAGAGAT GTTAAGTAAC CTGCCCAAGC CTCCCTCTGA	420
GCAATGGCAGA GGGAGGGTCC GAATGCGGAA AGTCTGGCTT CAGTGCCCCC ATCCTCTCGA	480
G	481

(2) INFORMATION FOR SEQ ID NO:569:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 472 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:

GAATTCGGCC TTCATGGCCT ACTCATCATT TGGAAAATAC TTGATGGCAG GAGAACTTGC	60
TTAAACTAA AGGTGGAGAA AGAGTAACT TCCAGGACAA CCCATTATAG CTCACTTCTT	120
ACCAACAAAG CAGTTTTTAT ACAGCACCTT AGGACTCATT TCTAATGTCA ACCCAGATGG	180
CCAGTAAAGG CAAGGGAAGA GGCTAAGTGA CTCACAAAAA TCTCTGATAT TGAGGTCTAA	240
TGTGAAGGCT ATAGATAGGA ATTCCCCACA AACTTCTAAT GAGGACTAAT ATGAACAGCA	300
AATTGGAGAA GACACCAAGG ACCTAATTTT AGTTTCACTA GCCGTGGGAC CTTAGAAAAA	360
AGACCATTG CTCTGGACTT TTGTTTCCCA AGCCATAAAA TGTGGAAGAA TCTTCACAAT	420
TTCAAGTTG TCATGTATAT TTCCCTTTTA CAGAGAAAGC TGAAGCCTCG AG	472

(2) INFORMATION FOR SEQ ID NO:570:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 487 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:

GAATTCGGCC TTCATGGCCT AGAAAGGATC AAGCTGATCA GAAGCGGGAG CTGCATTGAG	60
GGAAAAATAT GGCCAGAGAA GGCCTCACTG AGGAGGTGAC GTTGGTGATG CTGGAGCTCA	120
GATCTGAAGG GGAAGAAGGA AGCAGCCACA TATAGAAGTG AGGGAGGGGG CTTAGGCAAA	180
AGGAACAGCA AGCGGAGAGG CCCTGAGAAA GGAAAGGCTT GGCTCGCTCA CCTGCAAGGG	240
CCCCCTGGCT TGACATAGTG AGAAAGGTGT GAAGATGAAT TTGGAGAAAG GCAGGGACAG	300
ACCACAGGAG ACCTTAGATT TGATTCTGAG GGCGATGGGA TCCCTTGAGA GGATGCTGAG	360
CAGGGGAGAG ATGTGATCTC CTTTTCATTC TAACATGATC GCTGCAGCTG CTGCTGGAGA	420
ATGTTTGCAG GAGCGAGAGT AGAGACTGGG AAGTCTGTG CATCCTCTAA GCNACAGGCG	480
TCTCGAG	487

(2) INFORMATION FOR SEQ ID NO:571:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 456 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:

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GAATTCGGCC TTCATGGCCT AGAATAAATT GTGATACAAA AAAAAAAAAA AAAAAAGAGT      60
GTACACTATG AATGGGTTGG TCGTTTTCTT CCTGGCTTTT TTTCTTTTTA TTCAGAGTTA      120
GGAAATACTT TTATTTTSTA AAGGAAAATT CATCATAAAT TTGCGCTGGT ACTTTTGGAC      180
ACAGGATTCT TTCAGTGAAG CTTTGCCGGC CGGAAATCTC CATGGCCGGC CTGCGCTCTG      240
CCCGGTCTTC ACTGAAGCCT GCTGGGCTCT CTCCACCTAC TTGGTCCATC AGTCTGTGCT      300
TGGCTCATCC TAGCAACCTG GATCCCGCAC CCGTATGGC ACCGTGCTTG GCTGGAGGCT      360
GGTCCGAGCG TCCGTGACTA GCTTCCACCT TCGGCGCCAG CTTTGTGACA AGGGGAACGC      420
AGTGGCACCC AAAAATCTCG AGACATGAGA CTCGAG                                456

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(2) INFORMATION FOR SEQ ID NO:572:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:

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GAATTCTAGA CCTGCCTCGA GATGCCCCGAC TACTACAAAC CTCAGTACCT GCTGGACTTT      60
GAAGACCGCC TTCCCAGCTC GGTCCACGGC TCAGACAGTC TGTCCCTCAA CTCTTTCAAC      120
TCCGTCACTT CCACCAACCT GGAGTGGGAT GACAGTGCGA TTGCCCCATC TAGTGAGGAT      180
GGAGACCTCA CAGACACGGT CAGTGGTCCC CGCTCCACAG CCTCCGACCT GACCAGCAGC      240
AAGGCCTCCA CCAGGAGCCC CACCCAGCGC CAGAACCCCT TCAACGAGGA GCCGGCAGAG      300
ACTGTGTCCT CCTCTGACAC CACCCCGTG CACACCACCT CTCAGGAGAA GGAGGAGGCC      360
CAGGCCCTGG ACCCGCCGGA TGCCTGCACG GAGCTCGAG                                399

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(2) INFORMATION FOR SEQ ID NO:573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:

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GAATTCGGCC TTCATGGCCT AGATTGGGT TAGTGGTTTT CTTTATGAT GTTGAAAATG      60
TCACCCAACT GTTTCTGGG TTCCTTTGAA AAGCCAGCTG TCTGTCTGTC TGTTGTTCAT      120
GTCTGAAGGT GATGTGTCTT TACCTCTGGC TGCTTTAAGT ATCTTTTGCC TTTTCCCCT      180
TTGTGAATGT TTTTGCTGAA GTGTAACATA TACACAAAAG AGTGTGCAA TCATCAATGC      240
TTGATGATT CTCGAG                                256

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(2) INFORMATION FOR SEQ ID NO:574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:

GAATTCGGCT TCATGGCCTA GAATCATGCA TTTTCTTTTC TTTTTTTTTT TCCCGTTGGC	60
TTTGTCTATG CTGGTGGCAT CCAGGGCATT GCTTTGTCTC CCTGATTATG CCCAGGATTC	120
AAGGTCTTCT TATTTGTGGG GAGGCAGGCT GCCCACTGGG ACGGTTTTTA GTGTGTTTNC	180
CATTCCTGGC TCCCTCGAG	199

(2) INFORMATION FOR SEQ ID NO:575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:

GAATTCGGCC TTCATGJCCT AGGATTTGAA GAAGTTGGGA AAGCATTATG TAGATTAATA	60
TACTGCTTGG TTCCCTATCT ATGTGGAAGG TCATATTAGC TGCAATTATT TAATTTGCTG	120
TGTTATTTTG TGTTATATAA CACAAATATA TTTGTATATT AACTTCATTT TTAGTGTCAT	180
TTTTCTGTT GTATACAAA TGAACATC TTGTAATTAT TTTCAAATAT AGAAGTATAT	240
ACATTAGATG GATTTCCAAG ATTTTGTAAG NAAATCTTAA ATCAGTGTTT TGAGTTATTT	300
AATTTTAAA TTAATCTACA AATTATGCAC NACAACTAG CAACTCGAG	349

(2) INFORMATION FOR SEQ ID NO:576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:

GAATTCGGCC TTCATGGCCT ACAAATTTTG CTCACTTTCA TTAATCAGTT GCTCAGATAG	60
AAGGAAATGA CATCTGGTTC TGTCTTCTTC TACATCTTAA TTTTGGAAA ATATTTTCT	120
CATGGGGTGG ACAGGATGTC AAGTGCTCCC TTGGCTATTT CCCCTGTGGG AACATCACAA	180
AGTGCTTGCC TCAGCTCCTG CACTGTAACG GTGTGGACGA CTGCGGGAAT CAGGCCGATG	240
AGGACAACTG TGGAGACAAC AATGGATGGT CTCTGCAATT TGACAAATAT TTTGCCAGTT	300
ACTACAAAAT GACTTCCCAA TATCCTTTTG AGGCAGAAAC ACCTGAATGT TTGGTCGGTT	360
CTGTGCCAGT GCAATGTCTT TGCCAAGGTC TGGAGCTTGA CTGTGATGAA ACCAATTAC	420
GAGCTGTTCC ATCGGTTTCT TCAAATGTGA CTGCAATGTC ACTTCAGTGG AACTTAATAA	480
GAAAGCCCCT CGAG	494

(2) INFORMATION FOR SEQ ID NO:577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:

GAATTCGGCC TTCATGGCCT AGGCACGTTA AATTTAAAA GTTANAAAAA GAAAGATGCT	60
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TTTTGCAGCA GTTCCAGGGT AAACGGCCCC ATGCAACACA AACCTCGGG AAGGGCATT	120
CAGCCTTGCA GTGGGCCACG GAGTGCACCA CGCGGCGCTC AGCCCCCAG GGAAGCGATG	180
CCCCACATCG GGCCAGAAAC AAAAGGGGGT GAGATAAAGC ATGCTCGAG	229

(2) INFORMATION FOR SEQ ID NO:578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:

GAATTCGGCC TTCATGGCCT AAGGAGTTTG AGATATATTT AGGAAGCAGA GCCTATAAGA	60
CATGCTGATC ACTTGCATAC ATAACTGAG AGAACTAGAG GTATAGAAGA CTTCTAGAAC	120
TTGGAGAAAT TGGATGAATG GATGTATTGT TATTGATGTA ATGAACCTTA GAGGTGGGTG	180
GGATCAGAAA GATCTATTTG CTTTCAAAGG AAATGGGGAG TGGACAGGTA TGTGGCAGC	240
ATAAGAACTG GAATAACAGC ACATCTCATT CATGCCCTAA AAGAACGTGA AACTTTGAAT	300
GTACAGCAAT GGTATTCAAT AGGTATGACT TTGCCCTTAA AGGACATAGA CACCAGGGAT	360
GTTGCTAAAT ATCCTCCAAT GCACAACACA ACCCTCGAG	400

(2) INFORMATION FOR SEQ ID NO:579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:

GAATTCGGCC TTCATGGCCT ACGAGGACGA GGACGTCAAG GATAACTGGG ATGACGATGA	60
TGATGAAAAA AAAGAGGAAG CAGAAGTAA ACCAGAGGTA AAAATTTTCA AAAAGAAAAA	120
AATAGCAGAG AAGATAAAG AGAAAGAACG GCAACAGAAG AAAAGGCAAG AAGAAATTAA	180
AAAGAGGTTA GAAGAACCCG AAGAACCTAA AGTGCTAACA CCAGAAGAAC AATTAGCAGA	240
TAACTGCGG CTAAAGAAAT TACAGGAAGA GTCAGACCTC GAATTAGCAA AGGAACTTT	300
TGGTGTTAAT CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:

GAATTCGGCC TTCATGGCCT AAGCGAGGCC TGAGCCTCTG CGTCTAGGAT CAAAATGGTT	60
TCAATCCCG AATACTATGA AGGCAAGAAC GTCCTCCTCA CAGGAGCTAC CGGTTTTCTA	120
GGGAAGGTGC TTCTGAAAAA GTTGCTGAGG TCTTGTCCTA AGGTGAATTC AGTATATGTT	180
TTGGTGAGGC AGAAAGCTGG ACAGACACCA CAAGAGCGAG TGGAAGAAGT CCTAGTGGC	240

AAGCTTTTGTG ACAGATTGAG AGATGAAAAT CCAGATTTTA GAGAGNAAAT TATAGCAATC 300
AACAGCGAAC TCACCCAGAC TCGAG 325

(2) INFORMATION FOR SEQ ID NO:581:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:

GAATTCGNCC TTCATGNCCT ANGAGAAGNA CCCAGACCCC CCCAAGAAGG AGGAGGANCN 60
CCNNNGAGNC NCTNCTCCAG NCGGANGAGG AGCGCAAGGC CAAGTNCGCC AAGATNGAGG 120
CGGAGCNCGA GGCNTGNNC CAGGGCATCC GAGACAAGTA CGGCATCAAG AAGAAGGAGG 180
AGCGCGAGGC CGAGACCCAG ACGCCGCCAA GAAGGAGGAG GAGCGGCAGG AGGCGCTGCG 240
CCAGGCGGAG GAGGAGCGCA AGGCCAAGTA CGCCAAGATG GAGGCGGAGC GCGAGGCCGT 300
GCGCCAGGGC ATCCGAGACA AGTACGGCAT CAAGAAGAAG AAGAACGCTC GAG 353

(2) INFORMATION FOR SEQ ID NO:582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:

GARWYKCSS YYTTNANGGC TAGTCACTGG CAGGGCCACC CAGAAGCCCC GCAGATGACG 60
GAGCTGAGAA CAGGAATTN ACCTNCACGT GTTGCCATT CCTCANTGGA AAGTCCTTGG 120
GAGGTGGCTG GGCTCAGCCT GAGCTCAGGG CTTTTCGGTG GGGTTGGGGC AGGGGCAGGG 180
CGGGCNNTTG CAGGTGGCAC AGGCTTCATC AAGGCAGGAC ACGGGNTTCA TCAAGGCAGG 240
AGCCACAGCG CCCGAGCCCT GGCAGGGGAG GTAAGGCCCA GGATGGGGCA GGGCCGTGTG 300
CTCCTGGNAC GGACATCCTT NTCTGCCAGA GACCTGCTCC CCAAGCCCTG TCCCTCCCAA 360
TCCCCAGGCA GCCCACTCTG CCCTCCATAG ATGAATCTAA TATTGAATTT CTAGACCTGC 420
CTCGAG 426

(2) INFORMATION FOR SEQ ID NO:583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:

GAATTCGGCC TTCATGGCCT AAGAAAAGAA AGTAAGATTA TCTCCAGCCA AAATGTCAAC 60
CAAGAATTCT ACAGATCTAG TTGAATATGT TGACAAGAGT CATGCTTTTC TCCCCATCAT 120
TCCAAACACC CAGAGAGGTC AGCTAGAAGA CAGACTGAAC AACCAGGCAC GTACCATAGC 180
TTTCCTTCTT GAACAAGCCT TCCGCATCAA GGAGGACATC TCTGCTTGCC TGCAGGGGAC 240

CCATGGCTTT CGAAAAGAGG AATCGCTCGC CAGGAAGTTA CTGGAAGGCC ACATCCAGAC	300
CATCACCAGC ATCGTCAAAA AACTCAGCCA AAATATTGAG ATTTTAGAAG ACCAAATAAG	360
AGCTCGAG	368

(2) INFORMATION FOR SEQ ID NO:584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:

GGAATTCGGC CAAAGAGGCC TAAACGACTC TTGCCCCTGT TTCTTCTTGG CTTCCTTGC	60
GTAACAAGGA TGAAGGAGGT GGTTTAACTT TATTTTGTGC CTTTAACTTT TTAAAGTCTA	120
AAGTAAGTGC TTGAATCGGG TGGGTTTCA TTTTGTGCT TTCTCACCCC TCAGGTGGC	180
CCCTAACTTG GCCTCTCACC CTCGTGTCAG CTGTTAGACA CTGACTCAGT GGCTCAGAAT	240
ATGAAAGGCT CAGGAAGTAG CATGCTGGCC CCACCTCCCT GTCCCCATAC CTTAGCAGAG	300
CAGCTGCCCA GCAGGGCCTC CTTCTCTTTC CTAAGAGTTT ACTCCATCCA TGGTGGGTGT	360
CTTGGTAGGC CCGAGATACG AGAGGGAGTG CTGCTGTTAC AAGAATTAC AGTTGTCTC	420
TTCGGCACAA GCTCGAG	437

(2) INFORMATION FOR SEQ ID NO:585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:

GAATTCGGCC AAAGAGGCCT AGTGCAGAGT TGCAAGCAAG TTTATCAGAG ATACGCCATG	60
AAGTTCGTCC CCTGCCCTCCT GCTGGTGACC TTGTCCTGCC TGGGGACTTT GGGTCAGGCC	120
CCGAGGCAAA AGCAAGGAAG CACTGGGGAG GAATTCCATT TCCAGACTGG AGGGAGAGAT	180
TCCTGCNCTA TCGTCCCAG CAGCTTGGGG CAAGGTGCTG GAGAAGTCTG GCTTCGCGTC	240
GACTGCCGCA ACACAGACCA GACCTACTGG TGTGAGTACA GGGGGCAGCC CAGCAATGTG	300
CCAGGCTTTT GCTGCTGACC CCAAACCTTA CTGGAATCAA GCCCTGCAGG AGCTGAGGCC	360
CNTTCACCAT GCGTGCCAGG GGGCCCCGGT GCTTAGGCCA TCCGTGTGCA GGGAGGCTGG	420
ACCCCAGGCC CATATGCAGC AGGTGACTTC CAGCCTCAAG GGCAGCCCAG AGCCCAACCA	480
GCAGCCTGAG GCTGGGACGC CATCTCTGAG GCCCAAGGCC ACAGTGAAAC TCACAGAAGC	540
AACACAGCTG GGAAGGAATC TCGAG	565

(2) INFORMATION FOR SEQ ID NO:586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:

GAATTCGGCC AAAGGGCCTA CAGAATAGCG GTACCATGAT AGAATACTGC AATTGTGGTC	60
AGAATTACAG TATGCACAAA GAATTAATTA GCATTATTAA AGAGTCCTCA CTAAACATTT	120
CATATGATCA CACTGAAGAA CTGTAACATT CCATAGAGTG AAGTGGTTCA AATTTCTCTT	180
GGAATTTTAA CTTTGTGTGG CCTTATTTTA TGATCCTTTT CATATTTCTT TTGACTTAGA	240
GTATTAATAC ATGGCCAAAA TAATTTAGTT ACTACCTCAT ACAAACAATA TAATGGTTAC	300
TCGAG	305

(2) INFORMATION FOR SEQ ID NO:587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:

GAATTCGGCC AAAGAGGCCT AGTTGTTTTT AATGGCACAG GACTCTTCCA CTTTGTGGTC	60
CTCCTCTAGC ACAATACTGG ATGGCTGGGG CAAAAGATTA AAGGAAGTCT TTTCCACATC	120
ATTTTCTGCG TGTTCTCTCA ATCTTTTAC TAAATTGAT ACAAATTCCT CTATTCTTG	180
ATGATATTGC TTGAAATAG CATTTTCAT GAATAGAATC TGTAATATAG GTCCATCTAA	240
CTTAGTATCG TTCACCAATA TTCCACTCGG TCGAGTCAGA ATGTTCAATT TTCGTTAAG	300
TTCTTGATTG TCGGCGCGGA GCTGCTCGAT GGTCTCCACG CACTCGAG	348

(2) INFORMATION FOR SEQ ID NO:588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 486 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

GAATTCGGCC AAAGAGGCCT ACTCATGACA GGATGACAGT CACATTGGT AGACACCATC	60
AACCAATGAT CTCTAATTTG CGGCCCCCAA CAAGCAATGG GGTCTGTGG GCTACATCTG	120
GAATTTGAAA TGTCTCATGG AAATCATGTT CTACCCCTGG AGAAGGGTGG CTGCTTAGGT	180
GCTACTTAGG AAACCAGTCT GGCAGACCAG ATCTTCCCA ACTCAGGGGC TATGCGGGGA	240
GAAGTATTAG GAGCCCCTGA GCAGGAAGGA TGTACTTAGG AAGGCTACCG GGGATGGGGA	300
AGGGTAAAAG AGCTTAGAAG CCTGGGTGAA GTTTGGGTAG ACCAAAAACA GGAGGGAGGG	360
AGGGAGGATG TTCCCTTGA ATACAACTA GAGAAAAGCT TAGGGGANCA AGTCTTTTAA	420
TTTGGGGACA GTGAAGAGTT TCCTAAAAAT TCCTGGCCC CCAGGCCTTG GCTAAAAACC	480
CTCGAG	486

(2) INFORMATION FOR SEQ ID NO:589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:

GAATTCGGCC AAAGAGGCCT AATTGATTGT GATTAACCA	GATGTATGGA AAACAGTTTT	60
AAGTGTGTAG TGCATGTATC TCATAAGGTC CATTAGACG	TTCATTATTT TTCAATTGAT	120
GCGTCTTAAG CCCCACTTGA TGTGTGTTGT AGTGCAATTC	CACAGAAGGA TTCTGCACTG	180
TGGGATTGAG TTCATTTTGT TAATTGCATA ATACAACCCC	ATCGTGTTTC ATAGAAAATA	240
GTAAATACTC TTGCTTTTAT TCATTGGTAT TCTTTGATAT	TACTGAAGAA ATACCAAAGA	300
AGCAAAGGAG CAAAGAAATA CCAAAGAAGC AAAGGAGCAA	GTGAATAGTT CTTCAAACCT	360
TTACATATTA AGGGCACGAA TGTTCCTTGA AATGTGGACA	CATACTCGAG	410

(2) INFORMATION FOR SEQ ID NO:590:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:

GAATTCGGCC AAAGAGGCCT ACGGCCAAAG AGGCCTAATT	GAATTCTAGA CCTGCCTCGA	60
G		61

(2) INFORMATION FOR SEQ ID NO:591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:

GAATTCGGCC TTCATGGCCT ATCTAGACCC AAATATTTTG	AATATGTTAT CTTGTCTCTT	60
TTCTTTTGT TATATAGAGA GATTGATGCA TAAATCTGT	GTTGTATGA CTGTAATTCC	120
AAGTTTAGCG AAATTGTCCC TAGGACAACA CACCAACGGC	CATGAGCTGT CTCGGTCTCG	180
CAAGCTTAGT CTCCGATCCT GCCCACTCGA G		211

(2) INFORMATION FOR SEQ ID NO:592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:

GAATTCGGCC TTCATGCCTA GCCGGACCTG GTGCTCCTTT	CCTTGGTGCT GGGCTTCGTG	60
GAGCATTTTC TGGCTGTCAA CCGCGTCATC CCTACCAACG	TTCCCGAGCT CACCTTCCAG	120
CCCAGCCCCG CCCCCGACCC GCCTGGCGGC CTCACCTACT	TTCCCGTGGC CGACCTGTCT	180
ATCATCGCCG CCCTCTATGC CCGCTTCACC GCCCAGATCC	GAGGCGCCGT CGACCTGTCC	240
CTCTATCCTC GAG		253

(2) INFORMATION FOR SEQ ID NO:593:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 190 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:

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GAATTCGGCC TTCATGGCCT AAAGAAATGA AATAATATCT CTGAATTTTA GTCCATGTTT    60
TCAATGATTT CTGACTTTAT TATATTAAC TTTATTAATG ATCACAATTT ATTTTGTAAG    120
TTTTGCAGCC AAAGGGACAA TTTATTTTGT AAATTTGGGA TTCTATTTGC AAAATAGGGA    180
TCGACTCGAG                                         190
```

(2) INFORMATION FOR SEQ ID NO:594:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:

```
GAATTCGGCN TTCATGGCCT ACGGGGAACA GAGGATGGCG GAGGAGGGAA CACACAAGCA    60
GGAGCCCATG CAGCTGGGAG CCACTGAGAT CCCAGCTGGA GGAAGAGTGC CCTGGCACTG    120
AGGTCTAATG GCTGTCCAGC TGCTGCCCCA GGATGTGAGG GCAGGTGGTA GGCCATGAAG    180
GCCGATTGAA TTCTAGACCT GCCTCGAG                                         208
```

(2) INFORMATION FOR SEQ ID NO:595:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:

```
GAGCTATAAA ACAGAAATAC ATGCATAGCT GCAGAAACCA TGATAGGTAG AGGACTTTTC    60
TTTTGGTTTT GTTTGTTTT GTTTGTTTT GTTTTGGTT TTACAGAGAA GAGACTCGAG    120
```

(2) INFORMATION FOR SEQ ID NO:596:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:

GAATTCGGCC TTCATGGCCT AAGAAACCAA ATTAGCAGAC GGATAGAATA TAAAGCANGA	60
GGCAATACTT ATAGTGTATT AAGAACTTG CTAGACCCCA TCCAAATTAC TCAGTCTACT	120
GTTGGTTGAT AGAATTACTT TAGGAAGAGT ACGTTTTTCC TTGGAAATAC ACTGGAAGTG	180
GTACCAAACA AATCTAATAA AATGATGTTA AAGAGATTG CAGTAATTTT TATCNACTTT	240
CAGTTTGCAA ACTTTTATAA AGATATGAAA NGGACACTCG AG	282

(2) INFORMATION FOR SEQ ID NO:597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:

GGCCTTCATG GCCTAGACAC ATACAAAGAT AAGGCTTTGA TAAAATTCAA GAGTTATTTG	60
TATTTTGAGG AAAAAGACTT TGTGGATAAA GCAGAGAAGA GCCTGAAGCA GACTCCCAT	120
AGTGAGATAA TATTTTATAA AAATGGTGTC AATCAAGGTG TGGCTTACAA AGACATTCT	180
CGAG	184

(2) INFORMATION FOR SEQ ID NO:598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:

GAATTCGGCC TTCATGGCCT ACTTTGAGTT AAATAGAGAG TTGATTAAAT GCATATATTG	60
ACAGTTACTG ACTCAGTAAG CTTCATAATT CTAGGAATCA ATCACTGCTG ATTCATATGT	120
TTAGATATAT TCATTTCTGT CTTTCTGTTT CTTAGGCCAA AAAGAAAAAA GAAAACCAAT	180
ATTTAAGAGA AGAGAAAAAT GAAGACGGGA CATTTTGAAA TAGTCACCAT GCTGCTGGCA	240
ACCATGATTC TAGTGGACAT TTCCAGGTG AAGGCTGAAG TGTTAGACAT GGCAGATAAT	300
GCATTTGATG ATGAATACCT GAAATGTACG GACAGGATGG AAATTAAATA CGTCCCCCA	360
ATCCCTCGAG	370

(2) INFORMATION FOR SEQ ID NO:599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:

GAATTCGGCC TTCATGGCCT AAGACTCTTA GATCTAAAAG GAAACTGACT TGCCACCTTG	60
CCAGAGGAAT TCTTGAAATG TTTCTGCAGC CACTTGGCCT TGAAAATAAA GGGTGCAACT	120
CTCAATCTT GTTCTAACCC GGCTGGAGGA ACCACAAGAC CCAATGAAAT AGCATTTTCT	180
CTCCTTTTCC CAGCACTAGT ATATAACCTA TGAGGAACCC TTGTCTCTGA ATCTGCTCAG	240

```

CTTGAAATTT TGTCTCTGAA GGAAGAGAAT GATCTCAGCC CTAGTCTGAC AGTCCTAGAT    300
TTCTGTGAAA TAAGAGTATT CTTCAACTTA GTGCTCACAC TCACATACCA TGAGGGTTCT    360
CTGCAGAGGA CTCGAG                                     376

```

(2) INFORMATION FOR SEQ ID NO:600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:

```

GAATTCGGCC TTCATGGCCT AAGTCACTAT TTGGTAGCTG ACTTTGTGCC CTGATTAGAA    60
ACGTGGCTCC TTTTC.TGGT AGTTGTTCTT AGAACCTATC AACCTGCAGA GATTTTTATT    120
TTCATGGAAG GGAAGTGAAG GTTCTTTCTT TTGCTTCAGA CGGTACATC TTTAGATCCT    180
GAAGGGAGAG ATGCAGCTTG CTCTCTCCAG AGTCCAAATG CAGCAACAGA TTTTGCCTCC    240
ANGCAAGCAA GATATGCTAT AAAAACCTGC NACATTCCCT CACCAGCTCC TCTCTTTGAA    300
TTTTCGATGC CTCGATGGTC ATTTTCGAGAT GACAGCTTGT AGTGAGATAG CTGTGGCATT    360
GGAAGGGGGG AAGCATGCAC CATTTTCCCT AGGCCTTCC TGCTTTTGCT TGATAAGCAA    420
TTCTTTGAAT GGCATGTTCT CCACCTCTAG CCACCTTGTG TGTAGTCCCT ACTCTCGAG    479

```

(2) INFORMATION FOR SEQ ID NO:601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 483 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:

```

GAATTCGGCT TCATGGCCTA CACAGGCATA ACAGTCAGTC GGGAAAAGGT CACTGAAGTT    60
GCCCTTAAAG GTGAAGGGAC AGAAGAAGCT GAATGTAAAA AGGATGATGC TCTTGAAGT    120
CAGAGTCACG CTAAGTCTCC TCCATCCCCC GTGGAGAGAG AGATGGTAGT TCAAGTCGAA    180
AGGGAGAAAA CAGAAGCAGA GCCAACCCAT GTGAATGAAG AGAAGCTTGA GCACGAAACA    240
GCTGTTACCG NATCTGAAGA GGTCAAGTAAG CAGCTCCTCC AGACAGTGAA TGTGCCATC    300
ATAGATGGGG CAAAGGAACT CAGCAGTTTG GAAGGAAGCC CTCCTCCCTG CCTAGGTCAA    360
GAGGAGGCAG TATGCACCAA AATTCAAGTT CAGAGCTCTG AGGCATCATT CACTCTAACA    420
GCGGCTGCAG AGGAGGAAAA GGTCTTAGGA GAACTGCCA ACATTTTAGA AACAGGTCTC    480
GAG                                     483

```

(2) INFORMATION FOR SEQ ID NO:602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:

GGGCCGTGCA GGCAGTGAAT CGGAAAGTGG AGATGATGAA TGAAAAGAAC TTGGAGAAAG	60
GACTGGGGCGT GGACAGTGTG GACAAGGATG CCATGAACGC GGCCATCCAG CAGGCCATCA	120
AGGCCAGGCC GTCCATGTCT CCCAAGAAGG CGCCCCCAGC GCCTGCAAAG GAGGCCAGGA	180
ATGTCGTGGC CGTGGGTACT GGTGGCCGTG GGACCCACGA CCGAGACCCG AGTGAGAAAC	240
CACCCCGGCT CCAGTGGTTT GAACAGCAGG CGAAGAAGTT GGCAAAGCTA CTCGAG	296

(2) INFORMATION FOR SEQ ID NO:603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:

GAATTCGGCC TTCATGGCCT AGAACTTTT CATCTTTCCA AACAGAAATT CTATACCCAT	60
TAAACAGTAA CTCTCCCTTC ACCACTCTCC CCAACCCCGG AGACCTCTAT TCTATTTTCT	120
GTCTCTATAA ATTTGCCAT TTAGGTACC TCACATAAGT GAAATCATAT ATTTGCCCTT	180
TTGCATCTGG CTTATTTCAC TTAGCATGAT GTCTTCAAGG TTCATCCATG TGGTAGTAGC	240
AGAAATTTACT TCCTTTTAA GACTAGCATA CTCACACTGT TTTTGTGTT GTTTGTTGT	300
TTGTTGTTT TTGGGATGGA GTCTCACTCT GTTGCCAGG CTGTGGTGC GTGGTGCCAT	360
CTCGGCTCAC TGCGGCCTCT GCCTCCCGG TTCAAGTGAT TCTCATACCT CAGCCATCCC	420
TCGG	424

(2) INFORMATION FOR SEQ ID NO:604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:

GCGATTCGAT GTCCGTGCCC ACCTGGACCA CATCCCCGAC TACACCCCCC CCTCTGCTCA	60
CCACCATCTC CCCAGAACAG GAGTCGGACG AACGGAAGTG TAACTACGAG CGCTACAGAG	120
GCCTGGTGCA GAACGACTTT GCCGGCATCT CAGAGGAGCA GTGCCTGTAC CAGATCTACA	180
TTGATGAGTT GTACGGAGGC CTCCAGAGAC CCAGCGAAGA TGAGAAGAAG AAGCTGGCAG	240
AGAAGAAGGC TTCCATCGGT TATACCTACG AGGACAGCAC GGTGGCCGAG GTAGAGAAGG	300
CACTCGAG	308

(2) INFORMATION FOR SEQ ID NO:605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:

GGATGCTACA GAAATCACAG AAGAAAGCAG AACTTCTTGA TAATGAAAAA CCAGCTGCTG	60
---	----

TGGTTGCTCC	CATAACAACG	GGCTATACGG	TGAAAATCAG	TAATTATGGA	TGGGATCAGT	120
CAGATAAGTT	TGTGAAAATC	TACATTACCT	TAAGTGGAGT	TCATCAAGTT	CCCACTGAGA	180
ATGTGCAGGT	GCATTTTACA	GAGAGGTCAT	TTGATCTTTT	GGTAAAGAAT	CTAAATGGGA	240
AGAGTTACTC	CATGATTGTG	AACAATCTCT	TGAAACCCAT	CTCTGTGGAA	GGCAGTTCAA	300
AAAAAGTCAA	GACTGATACA	GTTCTTATAT	TGTGTAGAAA	GAAAGTGGAA	AACACAAGGT	360
GGGATTACCT	GACCCAGGTT	GAAAAGGAGT	GCAAAGAAAA	AGAGAAGCCC	TCCTATGACA	420
CTGAAACAGA	TCCTAGTGAG	GGATTGATGA	ATGTTCTAAA	GAAAATTTAT	GAAGATGGAG	480
ACGATGATAT	GAAGCGAACC	CTCGAG				506

(2) INFORMATION FOR SEQ ID NO:606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:

GGTGAATGA	AAGATATACC	TAGAACGCCA	TCTAGAGGGA	GAAGCGAATG	TGATTCTTCC	60
CCAGAACCGA	AAGCTTTGCC	TCAGACTCCT	AGGCCGAGGA	GTCGTTCTCC	ATCATCCCCA	120
GAGCTCAACA	ACAAGTGTCT	TACCCCCCAG	AGAGAAAGAA	GCGGGTCAGA	ATCATCAGTT	180
GATCAGAAAA	CTGTGGCTCG	GACTCCCCCTG	GGGCAGAGAA	GTCGTTCTGGG	ATCCTCTCAA	240
GAAGTTGATG	TGAAACCCAG	TGCATCCCCT	CAGGAAAGAA	GTGAGTCAGA	CTCTTCTCCA	300
GATTCTAAAG	CCAAGACACG	AACCCCACTT	CGGCAGAGGA	GTCGGTCTGG	ATCATCTCCA	360
GAGGTTGACA	GCAATCTCG	ACTATCCCCT	CGGCGCAGTA	GGTCTGTTTC	CTCCCCTGAA	420
GTGAAAGATA	AGCCAAGAGC	AGCACCAGG	GCACAGAGTG	GTTCTGATTC	CTCTCCTGAA	480
CCTAAAGCTC	CAGCCCCTCG	GGCCCTTCCC	AGACAACCTG	AG		522

(2) INFORMATION FOR SEQ ID NO:607:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:

GAATTCGGCC	TTCATGGCCT	AGGCGCACCA	AGAGCAGGGC	TGTGTGTGGG	AGGCTGCAGC	60
CAGGATTGCC	TCAGCTCCTC	CCCCTCAGGC	TGGGAGGATA	GCACAGGCTA	GGGGCTCGGG	120
GTGGAGGGTC	TCAGCTCTGC	TGCCCCCACC	CCAGTACTAG	CCTAGCTTCC	CAAGCTGTGG	180
CTTAGAGGAT	AGTTGGCTTC	CTGCCTCTCT	CCTCTAAAAT	AGCAAGTCTG	GGAAATCCTG	240
GGGTGAGTGG	AGTCACCCCA	CTCCCAGTTG	CTGGCAGAGA	CTGAGACTAA	AGCATCACTT	300
AATAAACCCC	CCAGCTCGAG					320

(2) INFORMATION FOR SEQ ID NO:608:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:

GAATTCGGCC TTCATGGCCT AGTTGTGTAT TCTTTTCTCT GTATCATATG TGATAGTGGG	60
GTAGTGCCAA ACATTGTTAA CTCTGATGAA TAATGTCTCT TTTGGTTAGA TCATTCTTAC	120
CTTACTGGTA TCTCTTACTG TTTCTTACC TAGTTATGCT GTTATTGCCT ATGGCTGTGC	180
CAGCTGCCCC AAGCTAACTT GTGAGAGGGA AGGTTGCCAG ACTGAGTTCT GCTACCACTG	240
CAAGCAGATA TGGCATCCAA ATCAGACATG CGATCTACTC GAG	283

(2) INFORMATION FOR SEQ ID NO:609:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:

GAATTCGGCC TTCATGGCCT ACACATGAGT GTGACCTCTG CCATGGGGAA ACACACACAG	60
AGATATCTAT ACATATATAC ATACATACAA ACATAGGCTA TCTTGGCACA CTAAATGCTA	120
AGCACTGTCT TAAGAGGTAG AGCTGGTGTG AGTGAAATTA ATGTTACATT TTCCAGCTGT	180
AAACAGACAT CTGCATTTCC TAGTGAGCTG CCAGGAGCCA GATTCGGGAA CCGTAACTGA	240
TGTGCCAGGA ATGGTGCAAT GATTCCCACT TCCAGGGATC TCTCGAG	287

(2) INFORMATION FOR SEQ ID NO:610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:

GAATGATAGG TCCTAGGTTT AACAGGGCCC TATTGACCC CCTGCTTGTG GTGCTGCTGG	60
CTCTTCAACT TCTTGTGGTG GCTGGTCTGG TCGGGGCTCA GACCTGCCCT TCTGTGTGCT	120
CCTGCAGCAA CCAGTTCAGC AAGGTGATTT GTGTTCGGAA AAACCTGCGT GAGGTTCCGG	180
ATGGCATCTC CACCAACACA CGGCTGCTGA ACCTCCATGA GAACCAAATC CAGATCATCA	240
AAGTGAACAG CTTCAAGCAC TTGAGACACT TGGAAATCCT ACAGTTGAGT AGGAACCATA	300
TCAGAACCAT TGAAATTGGG GCTTTCAATG GTCTGGCGAA CCTCAACACT CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:

GAATTCGCCT TCATGGCCTA ACCACATGAT CCTTCGTGTT TCTTGCCTTC CATTTCCCTT	60
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```

GGGTGGATGG TTGGGTAGGT GGGGTTTCCT GGTTTGGGGT TTCTCAGACA AGGGCCCTCT 120
AGGGAGGGTG CCCTGGACCC CCCACCACTC CTGGGCTGAG GAGCGTGCA CATGATGCCG 180
TTGGTGAGGT ACTGGAAGCC GTCATAGAGT TTGGTGGTGA TAGACCGCAT ACTGCCATCC 240
ACCATCTGCT CCACCAGCAG CTGCAGCTGC TCCTCAGTCA TGCTCATGTG GAACCTCTCT 300
TTGAGGTTNC GAATGGTGCT GGAGCCATGG AAGCAAGGAA GCTGAGAACC TTGTCCATGT 360
GTTTCCGAGC GGCAATCAGC CCTTGCAGCA TCA 393

```

(2) INFORMATION FOR SEQ ID NO:612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 645 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:

```

GAATTCGGCC TTCATGGCCT AGGCGGGTTA AAGTCACATT TTTAAAAAGG CTAAACTCTA 60
AATTGCTGTA TTTGCTCTCT CTGGAGATTA ACAAAGTGCT TGGTTTGCAG ATTTGCTGGT 120
ACGGTGATCT CAATGATATG ACCGAGGGTG GGAGGGATGT GAGGAGGGAA ATCGGCAAAA 180
CCCTGGCCAG CCAGCCAGCC AAGGTGACAC ACAGCCAGAG GGGGCTCCCC TCTCCTCCTG 240
CCGTCCGGCC ACGGCTCACC ACGCTGTCCA CTGGGAACGC GGCCCCGCGG CCCGCAGAGT 300
CAGGCGTGAG CTTGCCCTT TTCTGAAAGG GCCTCCGCCT GGGCAGGCGC CGGGGGGCAG 360
TCCTCGGGTC CCATGGCTTA GGAGCACAGC ACTGACGGCT GCAGTGGCTC GAAAGGCTGA 420
AATTCCACAT TGCTCTCTAG CGATCCCGCA CTGCTGCGAC GCCCTCGCTT CCCGGCTTCC 480
GAGAGGTCCT GCAGGGAGCT GCTGAGGGCG CTGCGCTTGA GGCCCTCACC GCTGGCATAG 540
CTGTCTCCA GGCAGGCCCG GCTCAGTGT TCCGTTGCCC GACTCCTTTT TGAGGCTAGA 600
GCACTGGGAC ATGCTGGGCC GCACGACGCC TTTCTGCTTC TCGAG 645

```

(2) INFORMATION FOR SEQ ID NO:613:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:

```

GCGATTGAAT TCTAGACCTG CCTCGCACCA CCCCAAATCC CACATCCTGC ACCCCTGCCT 60
CAGGCTTCCT GCCCTCAACC CCAATATTCT GAGCCTTCTC TTTTTTTTTG TTGTTTTTTT 120
GAGACAGAGT CTTGCTCTGT CTGTGCGACA GGCTGGAGAG CAGTGGCGCG ATCTCAACTC 180
ACTGCAACCT TCACCTCCCA GGTTCAGCA ATTCTCCTGT CTCAAGTGCC TAGATACCTT 240
GGTAATGATT CCATTGGCCC CACCATGCCC TGTCTGCCT TCCTGGCTGT GCCCAAGCTT 300
GGTCCCTGCC TGCCTGCCTC ACTCTCTGGG TCTCGAG 337

```

(2) INFORMATION FOR SEQ ID NO:614:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:

```

GAATTCGGCC TTCATGGCCT AGGTTT TAGA ATTTTATATG AAGTATCTTA TTTGATTTTC      60
ATAATAACCA TAGAAGATAG ATACTATTAT TATCCTTGGA TTATAGATGA AATTGAAGAT      120
TGCTTCGCGAG GTAGAGTTAA GATCCAGAAT GGTGACAAGA AGTATAATGT CTGCTTTTAT      180
GCCATAATAT ATCAGACTAT TCTGACTCAT TTAGATTACT TCAGGGCTAT CACTGAAGCT      240
TACAGTATTA TCACTACTGT GATACCCCTG CTCACACAAT TTGGTAAGTG TTTTGTATC      300
TTTTAGAACT TATACATTAG GCAGCAGCTA TCTGTTTGGT CAGCTGAAAG ACGGCCACAG      360
GATTTGCTTC TGGGTGGCCA TTAGCACCTT TCACCCATGC ACCAGAGAGA TACTTCCAGC      420
ACGAACTCGA G                                     431

```

(2) INFORMATION FOR SEQ ID NO:615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:

```

GAATTCGGCC TTCATGGCCT ACCAAAATTG TGCATACCCT TGGGATGAAA ATCATTGTAA      60
AGAAAAGAAA AAAGCAGGAN TATTTGAACA AATCACTAAA ACTCATGGAA CAATTTTGG      120
CATTACTTCA GGGATTGTCT TGGTCCTTCT CATTATTCT ATTTTAGTAC AAGTGAAACA      180
GCCTCGAAAA AAGGTCATGG CTTGCAAAAC CGCTTTTAAT AAAACCGGGT TCCAAGAAGT      240
GTTTGATCCT CCTCATTATG AACTGTTTTC ACTAAGGGAC AAAGAGATT CTGCAGACCT      300
GGCAGACTTG TCGGAAGAAT TGGACAATA CCAGAAGATG CGGCGCTCCT CCACCGCCTC      360
CCGCTGCATC CACGACCACC ACTGTGGGTC GCAGGCCTCC AGCGTCAAAC AAAGCAGGAC      420
CAACCTCAGT TCCATGGAAC TTCCTTCCG AAATGACTTT GCACAACCAC AGCCAATGCT      480
CGAG                                     484

```

(2) INFORMATION FOR SEQ ID NO:616:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:616:

```

GAATTCGGCC TTCATGGCCT AGCGTTCCTG GTTCCGTCCT TGTACATAAT ATTGTACAGC      60
ATTCAACCAC TTTTGTGCGAT CAGCAAAGTA GTCTCCAATG GCATTGTTGG CTTGTTCCAG      120
GAGACTGTCA TCTGCATCAC CAGATCCAGT TTTCAGGAGC TGGAGTACTC TAAACCAATC      180
CCCCAATTTC AGCCGGAGGC CAATAGCAAG ATCCCTTCTG TCCATCTCGA G               231

```

(2) INFORMATION FOR SEQ ID NO:617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 627 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:617:

```

GAATTCGGCC TTCATGGCCT ANAATGCTTC ATGAAGTNGC NGACAGGACT GACACAGCTN      60
AGCTTTTCTG ACTGATTTCG GGCCATGCAG TCTACCAAAG GGCTAGCTGT TGAGACAATG      120
AGGATCAGGG ACATTTGCCC TCGTTCTGAA TGTCCCCAGC CACAGTACNT ACATNGTTCT      180
TACATGTACC TTCCCCCTCG GTGACATTTT ATATTTTCCA AGNTGGCCAC ANCNGTTCCT      240
TTCCCTTTCT NNTNGNGNNG NACACTCACA CCGTCTCTG NGAGGTGAGG CCACATATTC      300
TCTTTTCTGG AATTGGGTG GGCCTGTGAC AATGGCAGGA CAATGCTGAG TGGCTATGTC      360
ATAAAGGCAA TACCCCTTCC ATCCAATTCT CTTGGGATGC TCATGTTTAG AATCCAGCCA      420
CCATGTTGTG AGGAAGCCCA CGTCACCTAT GAAGACCTAC ACAGAAAAGA CTCAAGGCCC      480
CAGGCACCTG AGCTGAAGGA TGAAAAAGAG TTAGTCAGCA GGGGAAATTG GGGAAAGGGT      540
ATCTGGTAGA AAGAAGGAAC AGCTTGTGCA GAGGTNCAGA GGCAAGAGAG AATTTGGCAT      600
ATTGCGGAAG CTGCAAAAGA TCTCGAG                                     627

```

(2) INFORMATION FOR SEQ ID NO:618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:

```

GAATTCGGCC TTCATGGCCT ACGACTTCAA AAATATGGGA ACACAGTTAG TTATTTTAC      60
ACAGTTCTTT TTGTTTTTGT GTGTGTGTGC TGTCGCTTGT CGACAACAGC TTTTGTGTTT      120
CCTCAATGAG                                     130

```

(2) INFORMATION FOR SEQ ID NO:619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 495 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:

```

GAATTCGGCC TTCATGGCCT ACTGGGGGAG GGGGAAGGATG TGGTTTGNAG AGNGGAAGCA      60
GAGTTTGGAA ACGCATGAGA GCAGAGCTTC GTGTGTTCCC ACCCTCANTG AGGANGTGTG      120
AGTGGGTGAG CATGTGAGAG TTGGGTGTTT CTACCCTCAG TGAGGAGGTG TGAGTGGGGG      180
TGCAATATAGA GGCAGTGCCT GCTGTGGGGT CACAACCTGGT GCATGCCAGC GCCAAAGGGA      240
CCTGTCTTTA GGGGTCAATT CAGCCAGCTC CTCCCATCAC ACATGACAGC TCCAAGCCTA      300
GAAGGGGCTC AGTGACAGGG CCAGGACAAG CCCTCAGGAC TGTGGCCTCC TGGCCCTTGG      360
TTCCCTGCCC CCACAACATG GTCTCCACAT GGCTGGCTGG CTGGCTGTCC CTGTGTGTGT      420
GTGACACACG GTGTGAGTGC AGGGCTGTGC CCGGGGTGGG AGGGTGTCTA TGTGGCACTG      480
ACTATCGAGC TCGAG                                     495

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(2) INFORMATION FOR SEQ ID NO:620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear